

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2005, 16:53:09 ; Search time 29 Seconds
(without alignments)
1341.109 Million cell updates/sec

Title: US-09-857-581B-66

Perfect score: 2389

Sequence: 1 MLELALGLXVIALFXHLRP.....AHSLVVCPLARIGVASKLS 521

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	94.2	521	3	US-08-948-564-14
2	944.5	39.5	512	4	US-09-672-785-4
3	940.5	39.4	506	4	US-09-672-785-2
4	921.5	38.6	506	4	US-09-672-785-8
5	651	27.2	513	3	US-09-351-229-4
6	637.5	26.7	508	4	US-09-142-108C-17
7	629	26.3	495	4	US-09-689-783A-2
8	626	26.2	512	4	US-09-142-108C-6
9	623	26.1	513	4	US-09-142-108C-15
10	618.5	25.9	496	3	US-09-292-768-2
11	618.5	25.9	496	3	US-09-292-768-66
12	616.5	25.8	496	3	US-08-881-784-1
13	616.5	25.8	500	3	US-09-292-768-4
14	616.5	25.8	500	3	US-09-292-768-68
15	616.5	25.8	512	4	US-09-142-108C-2
16	615.5	25.8	500	3	US-09-292-768-70
17	613.5	25.7	496	3	US-09-292-768-64
18	613.5	25.7	500	3	US-08-881-784-9
19	608	25.4	502	3	US-09-499-302A-2
20	605.5	25.4	496	3	US-09-172-339-6
21	602.5	25.2	471	3	US-09-126-420A-20
22	599.5	25.1	498	3	US-09-292-768-6
23	592	24.8	508	4	US-09-142-108C-19
24	590.5	24.7	500	4	US-09-142-108C-4
25	590	24.7	517	4	US-09-142-108C-21
26	583	24.4	516	3	US-08-948-564-12
27	574	24.0	496	1	US-08-313-075A-50

28	574	24.0	496	4	US-09-142-108C-41
29	572	23.9	502	3	US-09-499-302A-4
30	570.5	23.9	510	3	US-08-606-505B-66
31	570.5	23.9	510	3	US-09-616-990-66
32	567	23.7	476	4	US-09-142-108C-23
33	566.5	23.7	476	1	US-08-313-075A-30
34	564	23.6	523	3	US-08-606-505B-67
35	564	23.6	523	3	US-09-616-990-67
36	563.5	23.6	506	1	US-08-313-075A-38
37	563.5	23.6	506	3	US-08-606-505B-65
38	563.5	23.6	506	3	US-09-616-990-65
39	562.5	23.5	513	4	US-09-142-108C-42
40	559.5	23.4	529	4	US-08-615-192A-405
41	556.5	23.3	490	3	US-09-126-420A-16
42	556.5	23.3	520	2	US-09-091-432-2
43	556.5	23.3	520	4	US-09-387-663-2
44	556.5	23.3	520	4	US-09-214-139B-4
45	555.5	23.3	510	3	US-08-948-564-4

ALIGNMENTS

RESULT 1
US-08-948-564-14
; Sequence 14, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/948,564
; APPLICATION NUMBER: 800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-564-14

Query Match 94.2%; Score 2250; DB 3; Length 521;
Best Local Similarity 86.6%; Pred. No. 3.1e-273;
Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Db 1 MLELALGLVIALFLHLRPTTAKSALRHLNPPSPKRLPTIGHHLKDLHYAL 60
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Sequence 41, Appl
Sequence 4, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 23, Appl
Sequence 30, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 42, Appl
Sequence 405, App
Sequence 16, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 4, Appl

Qy 61 IDLSKKGHLPLFSXXFGSMPTVASTPELFLQXEXATSFTXRTQTSAXRXLTYDXXVA 120
Db 61 IDLSKKGHLPLFSXXFGSMPTVASTPELFLQXEXATSFTXRTQTSAXRXLTYDSSVA 120
Qy 121 XXPGPYWYFVRKLIIMNDLXNATTNNKRLPLRTOQTFRXLRXMAQXAEAKPLDXTBELL 180
Db 121 MVPGPYWYFVRKLIIMNDLXNATTNNKRLPLRTOQTFRXLRXMAQXAEAKPLDXTBELL 180
Qy 181 KWNSTYSMMXKLGBAEIIRDIARVILKXGEYSUTDFIXPLKXKLVKGYKRPDIIDILNKF 240
Db 181 KWNSTYSMMXKLGBAEIIRDIARVILKXGEYSUTDFIXPLKXKLVKGYKRPDIIDILNKF 240
Qy 241 DPVVERIVKRRXIVRRRNGEXXGKXSVGLDLEFAEDTETXIKTKXXIXGLVVD 300
Db 241 DPVVERIVKRRXIVRRRNGEXXGKXSVGLDLEFAEDTETXIKTKXXIXGLVVD 300
Qy 301 XFSAGDSTAXXTWALAEILNPNKVLXAXEEXYSVVGKDXLDEVDTONLPIYRAIVK 360
Db 301 XFSAGDSTAXXTWALAEILNPNKVLXAXEEXYSVVGKDXLDEVDTONLPIYRAIVK 360
Qy 361 ETRFMHPPPLPVKRXKXEBCKXNGXVYXPGALXXFNWQVXKXKXWDRPSEKRPERFLE 420
Db 361 ETRFMHPPPLPVKRXKXEBCKXNGXVYXPGALXXFNWQVXKXKXWDRPSEKRPERFLE 420
Qy 421 TXAEGEAXXLDLRCXHFQLLPFGSGRXWCPGVXLATSGXATLLASLIQCFDQVLGPOGO 480
Db 421 TXAEGEAXXLDLRCXHFQLLPFGSGRXWCPGVXLATSGXATLLASLIQCFDQVLGPOGO 480
Qy 481 ILKXGDAKVSMEERAGLTVPRASHLVCVPLARIGVASKLLS 521
Db 481 ILKXGDAKVSMEERAGLTVPRASHLVCVPLARIGVASKLLS 521

RESULT 2

US-09-672-785-4
; Sequence 4, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-4

Query Match 39.5%; Score 944.5; DB 4; Length 512;
Best Local Similarity 38.9%; Pred. No. 2.3e-109;
Matches 193; Conservative 94; Mismatches 182; Indels 27; Gaps 8;

Qy 33 PNPPSPXPRLPFTGHXHLKDKLLHYAXIDLKKGHLFSXXFGSMPTVASTPELPLKLF 92
Db 29 PSPPGPL-SLPITGHLLGLPR-LHHTFHFSLKYGFLQLKLGSI PCVVASTPELAREF 86

Qy 93 LOXKEATSPXRTQTSAXRXLTYDXXVAXXPYKXFKVFKLIIMNDLXNATTNNKRLPLR 152
Db 87 LKTYE-LAFSSRRKHSTAIDIVTYDSSFAFSYPYKXFKVFKLIIMNDLXNATTNNKRLPLR 145
Qy 153 TOOTIRKXLRMAQXAEAKPLDXTETELLKWNSTYSMMXKL-----GEAEIIRDIARE 204
Db 146 NLEVRSPQLLMMHKSFKGESVNVTDVLRVLTNSVISHMMLSIKCSDEDEGDAEAARTVIRE 205
Qy 205 VLKXGEYSUTDFIXPLKXKLVKGYKRPDIIDILNKFDPVVERIVKRRXIVRRRNGEXX 264
Db 206 VTQIFGEFVDITIIWFCCKFDLQGIKKRSEDIQRRYDALLEKTIISDRER--SRQNRDKH 263
Qy 265 EG---EXSGVXKLTLEFAEDTETXIKTKXXIXGLVVDXFSAGDSTAXXTWALAEIL 321
Db 264 GGGNNEAKDFLMDLDDVMESGTEVKFTREHLKALILDFFTAGTDTTATATWALAEIL 323
Qy 322 NPNKVLXAXEEXYSVVGKDXLDEVDTONLPIYRAIVKTFRMHPPPLPVKRXKXEBCK 381
Db 324 NPNVLKKAQEEISRIGTKRIVQESDAPDLPVLQAIKETFRHLHPPIMLSRKSTSDCT 383
Qy 382 INKXVXPEGALXXFNWQVXKXKXWDRPSEKRPERFLETYXAGEAXXLDLRCXHFQLLP 441
Db 384 VNGYKIQAKSLLEFVNWISIGRNPYWESEPMERPERFLEKGRE----SIDVKQGHFELLP 439
Qy 442 FSGRXWCPGVXLATSGXATLLASLIQCFDQVLGPOGOQLKXDAKVSMEERAGLTVPR 501
Db 440 FGTRRGCPGMLAIGEVWSIIIGTMVQCDF-----WKLADSGNNVDMTERSGLTAPR 492
Qy 502 AHSVLVCVPLARIGVAS 517
Db 493 AFDLCRLYPRVDPAT 508

RESULT 3

US-09-672-785-2
; Sequence 2, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-2

Query Match 39.4%; Score 940.5; DB 4; Length 506;
Best Local Similarity 39.8%; Pred. No. 7.1e-109;
Matches 196; Conservative 86; Mismatches 185; Indels 25; Gaps 9;

Qy 30 RHLNPPSPXPRLPFTGHXHLKDKLLHYAXIDLKKGHLFSXXFGSMPTVASTPELPLF 89
Db 24 RRKTRPPGGL-ALPLIGHLLGLPK-LHHTFHQFSQRYGFLIQLGLSGVPCVVASTPELA 81

Qy 90 KLFQXKEATSFYTRFQTSAXRXLTYDXXVAXXPGPYWFXVRKLIIMDLXNATTVNXLRL 149
Db 82 REFLKTHE-LDFSRKHSSTAIIDIVYDSSFAFAPYGPYKFIKKLCTYELLGARNLGHFQ 140
Qy 150 PLRTQOIRKXLRMAQXAEAKPLDXTEELLKXNXTXSMXKL-----GEAEERDI 201
Db 141 PIRALEVNSFURILYEKTEQKQSVNVTEELVKLTNSVISHMMLSGIRCSGTEGEAEVARTV 200
Qy 202 AREVLKIXGESYSLDFIXPLKXKLVGKYEKRIDDILNKFPDVPVVERVIKRRXIVRRRXNGX 261
Db 201 IREVTQIFGEFVSDIWLCKNFDFQGIKRSSEDIQRYDALLEKIITDREK--QRRTHGGGG 259
Qy 262 EXXEGESGVKLDYLLFAEDETXEIKITKXIXGLVVDXPSAGXSTAXXTWALAEILI 321
Db 260 GGGGGEVKD-FDMLLDVMESEKSEVEFTRHLKALILDFFTAGTDTTATTEWAIJAEI 318
Qy 322 NNPLVXXABEEXSVVGVKDXLVDVDTQNLPIYRAIVKETFRRMHPPLPVVKRKCXEECX 381
Db 319 SNPNVLKKAQEEEMDKVIGSQRLQESDAPNLPYLALIKETFRHLPPIMLTRKSIISDVV 378
Qy 382 INGXXPEGALXXFNVMQVGDXXKXWDPRSEXPFRFLETXAEGEAXKXLDLGRGXHFOLLP 441
Db 379 VNGYTIKATLLFVNLMSGRNPNYMNPMFRPERFLEXG----TGSIDVKGQHFELLP 434
Qy 442 FGSGRXWCPGVXLATSGXATLLASLIQCFLQVLGPGQQLKGDAXKVSMEERAGLTVPR 501
Db 435 FGTRRGCPGMLLMQBELSFIIGAMVQCFDWKL--PDGV-----KSVDMTERPGLTAPR 486
Qy 502 AHSLVCVPLARI 513
Db 487 ANDLVQCLVPRI 498

RESULT 4

US-09-672-785-8
; Sequence 8, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takasaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Perilla frutescens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to directly convert flavanone to flavone
US-09-672-785-8
Query Match 38.6%; Score 921.5; DB 4; Length 506;
Best Local Similarity 38.9%; Pred. No. 1.7e-106;
Matches 190; Conservative 91; Mismatches 183; Indels 25; Gaps 8;
Qy 33 PNPPSPXPRLPFGHXHLLKXLLHYAXIDLKXKGGPLFSXXFGSMPTVASTPELPLKLP 92
Db 27 PYPGPPFP-LPIIHLHLGPR-LHQTFHDLISQRYGMLQMLRGLSIRCVIAASPELAKEC 84

Qy 93 LOXXEATSFYTRFQTSAXRXLTYDXXVAXXPGPYWFXVRKLIIMDLXNATTVNXLRLPLR 152
Db 85 LKTHELV-FSSRKHSSTAIIDIVYDSSFAFAPYGPYKFIKKLCTYELLGARNLAHFQPIR 143
Qy 153 TQOIRKXLRMAQXAEAKPLDXTEELLKXNXTXSMXKL-----GEAEERDIARE 204
Db 144 TLEVKSFLQILMRKSGESGFNVTEELVKLTNSVISHMMLSIKRSCTESEAEAAARTVIRE 203
Qy 205 VLKIXGESYSLDFIXPLKXKLVGKYEKRIDDILNKFPDVPVVERVIKRRXIVRRRXNGEXX 264
Db 204 VTQIFGEFVSDIWLCKNFDFQGIKRSSEDIQRYDALLEKIITDREK--QRRTHGGGG 261
Qy 265 EGXSGVXLDTLLFAEDETXEIKITKXIXGLVVDXPSAGXSTAXXTWALAEILNPP 324
Db 262 GCGEAKDFLMDLIMESGKAEVKFTRHLKALILDFFTAGTDTTATVCEWAIJAEVINNP 321
Qy 325 XVLXXABEEXSVVGVKDXLVDVDTQNLPIYRAIVKETFRRMHPPLPVVKRKCXEECXING 384
Db 322 NVLKKAQEEIANIVGFRILQESDAPNLPYLALIKETFRHLPPIMPLARKSISDCVLDG 381
Qy 385 XVXPEGALXXFNVMQVGDXXKXWDPRSEXPFRFLETXAEGEAXKXLDLGRGXHFOLLPPGS 444
Db 382 YNIPANTLLFVNLMSGRNPNKIWDYPTAFQPERFLEX-----EKAAIDVKGQHFELLPGT 437
Qy 445 GRXWCPGVXLATSGXATLLASLIQCFLQVLGPGQQLKGDAXKVSMEERAGLTVPRAHS 504
Db 438 GRRGCPGMLLAIQEVIIIGTMIQCDFWKL--PDG-----SGHVDMAERPGLTAPRETD 489
Qy 505 LVCVPLARI 513
Db 490 LFCRVVPRV 498

RESULT 5

US-09-351-229-4
; Sequence 4, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
US-09-351-229-4
Query Match 27.2%; Score 651; DB 3; Length 513;
Best Local Similarity 32.6%; Pred. No. 1.6e-72;
Matches 164; Conservative 89; Mismatches 200; Indels 50; Gaps 13;

Qy 35 PPSPXPRLPFGHXHLLKXLLHYAXIDLKXKGGPLFSXXFGSMPTVASTPELPLKLPQ 94
Db 29 PPGPKP-WPTIGNLNLM-GELPHRSMNELSKRYGPLMLQMLWFGSLPVVVGASAEMAKFLK 86
Qy 95 XXEATSFYTRFQTSAXRXLTYD--XXVAXXPGPYWFXVRKLIIMDLXNATTVNXLRLPRT 153
Db 87 TNDL-AFSDRPRFVAVGKYTAYDCSLWAPPEPVLROARRICATELFSATRLSEFHIRD 145
Qy 154 QOIRKXLRMAQXAEAKPLDXTEELLKXNXTXSMXKLGE----- 194
Db 146 EEVVVMRLQLRQAAGRTVRLRDYQLML--ALGVISRLVGLKKYVMEEAADGEGSDAPAIT 203
Qy 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIDDILNKFPDVPVVERVI---KKR 251
Db 204 PASFRENVDEFFALHGAFFNIGDYTPMLDWLDLQGYVARMKMKARFGRLERVLDVHNER 263

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2005, 17:33:00 ; Search time 874 Seconds
(without alignments)
3628.930 Million cell updates/sec

Title: US-09-857-581B-66

Perfect score: 2389

Sequence: 1 MLLELALGLXLVLFHXLRP.....AHSIVCVPLARIGVASKLS 521

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Published Applications NA:*

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20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	94.5	2258	1756	16	US-10-171-174A-9
2	94.5	2258	1756	16	US-10-104-706-1
3	94.5	2256	1709	17	US-10-310-154-367
4	94.2	2250	1824	18	US-10-659-755-1
5	89.2	2130	1974	18	US-10-739-930-3497
6	94.5	2130	1974	17	US-10-411-115-3
7	94.5	2130	1974	18	US-10-411-225-3
8	94.5	2130	1974	17	US-10-411-115-1
9	94.5	2130	1974	18	US-10-411-225-1
10	92.5	2130	1974	17	US-10-411-115-7
11	92.5	2130	1974	18	US-10-411-225-7
12	91.5	2130	1974	17	US-10-424-599-6882
13	91.5	2130	1974	18	US-10-424-599-78567
14	87.0	2130	1974	17	US-10-424-599-120588
15	84.3	2130	1974	18	US-10-424-599-101968
16	80.5	2130	1974	18	US-10-437-963-48274
17	76.5	2130	1974	18	US-10-437-963-21012
18	73.0	2130	1974	18	US-10-437-963-67133
19	71.7	2130	2278	17	US-10-424-599-100510
20	70.5	2130	2278	17	US-10-424-599-115417
21	69.3	2130	2278	17	US-10-424-599-115417
22	69.3	2130	2278	17	US-10-424-599-115417
23	69.3	2130	2278	17	US-10-424-599-115417
24	69.3	2130	2278	17	US-10-424-599-115417
25	69.3	2130	2278	17	US-10-424-599-115417
26	69.3	2130	2278	17	US-10-424-599-115417
27	69.3	2130	2278	17	US-10-424-599-115417
28	69.3	2130	2278	17	US-10-424-599-115417
29	69.3	2130	2278	17	US-10-424-599-115417
30	69.3	2130	2278	17	US-10-424-599-115417
31	69.3	2130	2278	17	US-10-424-599-115417
32	69.3	2130	2278	17	US-10-424-599-115417
33	69.3	2130	2278	17	US-10-424-599-115417
34	69.3	2130	2278	17	US-10-424-599-115417
35	69.3	2130	2278	17	US-10-424-599-115417
36	69.3	2130	2278	17	US-10-424-599-115417
37	69.3	2130	2278	17	US-10-424-599-115417
38	69.3	2130	2278	17	US-10-424-599-115417
39	69.3	2130	2278	17	US-10-424-599-115417
40	69.3	2130	2278	17	US-10-424-599-115417
41	69.3	2130	2278	17	US-10-424-599-115417
42	69.3	2130	2278	17	US-10-424-599-115417
43	69.3	2130	2278	17	US-10-424-599-115417
44	69.3	2130	2278	17	US-10-424-599-115417
45	69.3	2130	2278	17	US-10-424-599-115417

ALIGNMENTS

RESULT 1

US-10-171-174A-9
; Sequence 9, Appli
; Publication No. US20030150012A1
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; TITLE OF INVENTION: OF AN ISOFLAVONOID-PRODUCING PLANT
; FILE REFERENCE: B1452 US NA
; CURRENT APPLICATION NUMBER: US/10/171.174A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,981
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max

SEQUENCE 9, Appli
Sequence 1, Appli
Sequence 367, App
Sequence 1, Appli
Sequence 3497, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 689, Ap
Sequence 78567, A
Sequence 120588,
Sequence 101968,
Sequence 48274, A
Sequence 21012, A
Sequence 67133, A
Sequence 100510,
Sequence 115417,
Sequence 1264, Ap
Sequence 24949, A
Sequence 89837, A
Sequence 2248, Ap
Sequence 94744, A
Sequence 38374, A
Sequence 12, Appli
Sequence 27875, A
Sequence 94743, A
Sequence 16, Appli
Sequence 3724, Ap
Sequence 259, App
Sequence 197, App
Sequence 261, App
Sequence 195, App
Sequence 193, App
Sequence 46212, A
Sequence 2618, Ap
Sequence 5, Appli
Sequence 14, Appli
Sequence 149, App
Sequence 2607, Ap
Sequence 10169, A
Sequence 191, App

US-10-171-174A-9

Alignment Scores:

Pred. No.: 0 Length: 1756
Score: 2258.00 Matches: 452
Percent Similarity: 86.76% Conservativity: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.52% Indels: 0
DB: 16 Gaps: 0

US-09-857-581B-66 (1-521) x US-10-171-174A-9 (1-1756)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 67 ATGTTGCTGGAACATGACCTGGTTGTTGTTGTTAGCTTTGTTCTGACCTTGGCTGCC 126
QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 127 ACACCAAGTGCAAAATCAAAAGCACTTCGCACCTCCCAACCTCCAAAGCCCT 186
QY 41 ArgLeuProPheLeuGlyHis***HisLeuLeuLysAspLysLeuHisTyrAla*** 60
DB 187 CGTCTCCCTTCATGTGCCACCTTCACCTCTTAAAGATAAACTTCTCCACTATGCATC 246
QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
DB 247 ATCGATCTCTCAAAAAGCATGGCCCTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 306
QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
DB 307 GTCTGTGCTCCACCCCTGAGTTGTTCAAGCTCTCTCCCAACCCACGAGCAACTTC 366
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
DB 367 TTCAACACAGGTTTCCAAACCTCTGCCATAAGACGCTCTCTTACGCAACTCTGTGGCC 426
QY 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140
DB 427 ATGTTTCATTCGGACCTTCTGGAAGTTCTGAGGAGCTCATCATGACGACCTTCTC 486
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
DB 487 AAGGCCACCCCGTCAACAGCTCAGGCTTTGAGGACCCCAACAGATCCGCAAGTCTCTT 546
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
DB 547 AGGGTTATGGCCCAAGCGGAGGCGCCAGAAAGCCCTTGACGTCCCGAGGAGCTTCTC 606
QY 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
DB 607 AATGGACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGGATCAGAGAC 666
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
DB 667 ATCGCTCGCAGGTTCTTAAGATCTTCGCGCAATACAGCCTCACTGACTTTCATCTGCCT 726
QY 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
DB 727 TTGAAGTATCTCAAGGTTGGAAGTATGAGAGAGGATGATGATGATGATGATGATGATG 786
QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArg***Asn 260
DB 787 GACCTGTCTGTAAGGCTCATCAAGAGCGCGCTGAGATCGTCAGAAGGAGAAAGAAC 846
QY 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
DB 847 CGAGAAGTTGTTAGGCGGAGCGCCAGCGCGCTTCTCTCGACACTTCTCTGAAATTCGCT 906
QY 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
DB 907 GAGGACGAGACCATGAGATCAAAATACCAAGGAGCAAAATCAAGGCGCTTGTGTGCGAC 966
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320

DB 967 TTTTCTCTGAGGACAGATTCCACAGCGTGGCAACAGAGTGGCATTTGGCAGAGCTC 1026
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 1027 ATCAACAATCCAGGCTGTTGCAAAAGGCTCGTGAGGAGGTCTACAGTGTGTTGGGCAAA 1086
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1087 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCTTACATTAGGGCCATTGTGAAG 1146
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
DB 1147 GAGACATTCCGAATCACCCACCTCCAGTGGTCAAAAGAAAGTGCACAGAGAGTGT 1206
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
DB 1207 GAGATTAAATGGGTATGTGATCCAGAGGAGCAITGGTCTTTTCAATGTTTGGCAAGTA 1266
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1267 GGAAGGACCCCAATACTGGGACAGACCATCAGAAATCCGTCCGAGAGGTCTTTAGAA 1326
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1327 ACTGGTGTCTGAAGGGAAGCAGGCGCTCTTGATCTTAGGGGCCAGCATTTCCAACTCCTC 1386
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1387 CCATTGGGTCTGGGAGGAGAAATGTCCCTGTGTGCAATTTGGCTACTTCAGGAATGGCA 1446
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1447 ACATCTTTCATCTCTTATCCAAATGCTTTGACCTGCAAGTCTGGGCCCTCAAGCAAA 1506
QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
DB 1507 ATATTCAAGGTGATGATGCCAAAGTTAGCTGGAAGAGAGAGAGCTGGCCCTCACAGTTCCA 1566
QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
DB 1567 AGGGCACATAGTCTCGTTTGTGTTCACCTTGCAAGGATCGCGTTGCACTAAACTCCTT 1626
QY 521 Ser 521
DB 1627 TCT 1629
RESULT 2
US-10-104-706-1
; Sequence 1, Application US/10104706
; Publication No. US20030167507A1
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; APPLICANT: Lu, Guihua
; APPLICANT: Xu, Hu
; APPLICANT: Ruff, Richard
; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and its Use
; FILE REFERENCE: BB1468 US NA
; CURRENT APPLICATION NUMBER: US/10/104,706
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278379
; PRIOR FILING DATE: March 23, 2001
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-104-706-1
Alignment Scores:
Pred. No.: 0 Length: 1756

Db	1027	ATCAAAACAAATCCCAAGGCTGTTGCCAAAAGGCTCGTGAGAGAGCTCTACAGTGTGTGGGCAAA	1086
QY	341	Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys	360
Db	1087	GATAGACTCGTTGACGAGAGTTGACACTCAAAACCTTCCTTACATTAGGGCCATTGTGAAG	1146
QY	361	GluThrPheArgMetHisProLeuProValValLysArgLysCys***GluGluCys	380
Db	1147	GAGACATTCGGAATGCACCCACCACTCCCAAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT	1206
QY	381	***IleAsnGly***Val***ProGluGluAlaLeu*****PheAsnValTrpGlnVal	400
Db	1207	GAGATTAAATGGGTATGTGATCCAGAGGGAGCAATTGGTTCTTTTCAATGTGTGGCAAGTA	1266
QY	401	Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu	420
Db	1267	GGNAGGACCCCAATACATCGGACAGACCATCAGAAATTCGTTCCCGAGAGGTTCTTAGAA	1326
QY	421	Thr***AlaGluGluGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu	440
Db	1327	ACTGGTGTCTGAAGGGGAAGCAGGGCCCTCTTTGATCTTTAGGGCCAGCATTTCCAACCTC	1386
QY	441	ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala	460
Db	1387	CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGTGTCAATTTGGCTACTTTCAGGAATGGCA	1446
QY	461	ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGluProGlnGlyGln	480
Db	1447	ACACTCTTTGGCATCTCTTATCCAAATCTTTGACCTGCAAGTGTGGGCCCTCAAGGACAA	1506
QY	481	IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro	500
Db	1507	ATATTGAAAGGTGATGATGCCAAAGTTAGCATGGAAAGAGAGAGCTGGCCTCACAGTTCCA	1566
QY	501	ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu	520
Db	1567	AGGGCACATAGTCTCGTTTGTGTTCACCTTGAAGGATCGGCGGTTCATCTAAACTCCTT	1626
QY	521	Ser 521	
Db	1627	TCT 1629	

RESULT 3

US-10-310-154-367

: Sequence 367, Application US/10310154

: Publication No. US20030233670A1

: GENERAL INFORMATION:

: APPLICANT: Edgerton, Michael D

: APPLICANT: Chomet, Paul S.

: APPLICANT: Adams, Thomas H

: APPLICANT: Ruff, Thomas G.

: APPLICANT: Agarwal, Ameeta K.

: APPLICANT: Ahrens, Jeffrey E.

: APPLICANT: Ball, James A.

: APPLICANT: Banu, G.

: APPLICANT: Bell, Erin

: APPLICANT: Boddupalli, Raghava

: APPLICANT: Deikman, Jill

: APPLICANT: Deng, Molian

: APPLICANT: Dong, Jinzhao

: APPLICANT: Duff, Stephen M.

: APPLICANT: Galligan, Meghan M.

: APPLICANT: Hinchey, Brenda S.

: APPLICANT: Huang, Shihshieh

: APPLICANT: Johnson, G. Richard

: APPLICANT: Jung, Vincent

: APPLICANT: Kretzmer, Keith A

: APPLICANT: Laccetti, Lucille B.

: APPLICANT: Lai, Chao-Qiang

: APPLICANT: Lee, Gary

: APPLICANT: Lin, Jie-Yi

: APPLICANT: Liu, Jingdong

APPLICANT: Lu, Bin
 APPLICANT: Luethy, Michael M.
 APPLICANT: Lund, Adrian
 APPLICANT: Madison, Linda L.
 APPLICANT: Malloy, Kathleen A.
 APPLICANT: McKiel, Christine L.
 APPLICANT: Miller, Philip W.
 APPLICANT: Padmavathi, Manchikanti
 APPLICANT: Parnell, Laurence D.
 APPLICANT: Start, William G.
 APPLICANT: Tennesen, Dan
 APPLICANT: Vidya, K.R.
 APPLICANT: Wang, Haiyun
 APPLICANT: Xin, Zhanguo
 APPLICANT: Xu, Nanfei
 APPLICANT: Yang, Chunzhi
 APPLICANT: Zeng, Xiaoping
 APPLICANT: Zhang, Qiang
 APPLICANT: Zhao, Yajuan
 APPLICANT: Zhou, Li

TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants

FILE REFERENCE: 38-15(52796)B

CURRENT APPLICATION NUMBER: US/10/310,154

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/337,358

PRIOR FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 736

SEQ ID NO 367

LENGTH: 1709

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

NAME/KEY: CDS

LOCATION: (45)..(1607)

OTHER INFORMATION:

US-10-310-154-367

Alignment Scores:

Pred. No.: 0 Length: 1709
 Score: 2256.00 Matches: 452
 Percent Similarity: 86.76% Conservative: 0
 Best Local Similarity: 86.76% Mismatches: 69
 Query Match: 94.43% Indels: 0
 DB: 17 Gaps: 0

US-09-857-581B-66 (1-521) x US-10-310-154-367 (1-1709)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu**ValLeuAlaLeuPhe***HisLeuArgPro 20
 Db 45 ATGTTGCTTGAACCTGCACCTGGTTTATTGTTTGGCTCTGTTCTGCACCTTGGCTGCC 104
 Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro 40
 Db 105 ACACCCACTCGAAATCAAAAGACATTGCGCATCTCCCAACCCACCAAGCCCAAGCCT 164
 Qy 41 ArgLeuProPheLeuGlyHis***HisLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 165 CGTCTTCCCTTCATAGACACCTTCATCTCTTAAAGACAAACTCTCCACTACGCACTC 224
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 225 ATCGACCTCTCCAAAAACATGGTCCCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 284
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 285 GTTGTGGCTTCCACACAGAAATGTTCAAGCTCTTCTCCAAACGACGAGGCAACTTCC 344
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 345 TTCAACACAGAGTTCCAAACCTCAGCCATAAGCGCTCACCCTATGATAGCTCAGTGGCC 404
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140

Db 405 ATGTTCCCTTCGACCTTACTGGAAGTTCTGTGGAAGCTCATCATGACGACCTTCTC 464
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 465 ACGCCACCACTGTAAACAAGTTGAGCGCTTTGAGGACCCACAGATCCCAAGATTCCTT 524
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 525 AGGTTATGGCCCAAGCGCAGGACAGAGAGCCCTTGTGACCTGACCGAGGAGCTTCTG 584
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 Db 585 AAATGACCAACACAGACCATCTCCATGATGATCTCGCGAGGCTGAGGAGATCAGAGAC 644
 Qy 201 IleAlaArgGluValLeuLysIle***GlyLysTyrSerLeuThrAspPheIle***Pro 220
 Db 645 ATCGCTCGGAGGTTCTTAAGATCTTTGGGAATACAGCCCTCACTGACTTCACTTGGCCA 704
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 705 TTGAAGCATCTCAAGGTTGGAAGTATGAGAGGATCGACGACATCTTGAACAAGTTC 764
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 Db 765 GACCTCTGCTGTTCAAAAGGCTCATCAAGAAGCGCGTGAGATCGTGAGGAGGAGAAAC 824
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuPheAla 280
 Db 825 GGAGAGGTTGTTGAGGAGTGGTCAAGCGGTTTCTTGTGACACTTGTGTTGATTCGCT 884
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
 Db 885 GAGGATGAGACCATGAGATCAAAATCACCAGGACCATCAAGGCTCTTGTGTGCGAC 944
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 Db 945 TTTTCTCGGCGAGAAACAGACTCCACAGCGGTGCGCAACAGAGTGGGCATTGGCAGAACTC 1004
 Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 Db 1005 ATCAACAATCCTNAGGTGTTGNAAGGCTCTGAGGAGGTCTACAGTGTGTGGGNAAG 1064
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 Db 1065 GACAGACTTGTGACGAAGTTGACACTCAAAACCTTCTTACATTAGACGAATCGTGAAG 1124
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 Db 1125 GAGACATTCGCAATGCCCGCCACTCCAGTGGTCAAAAGAAAGTGCACAGAGAGTGT 1184
 Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
 Db 1185 GAGATTATGATATGATGATCCAGAGGAGGAGCATTAATCTCTCTCAATGATGGCAAGTA 1244
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 Db 1245 GGAAGAGACCCCAATACTGGGACAGACCATCGAGTTCGCTCCTGAGAGGTTCTTAGAG 1304
 Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 Db 1305 ACAGGGGCTGAAGGGAAGCAGGGGCTCTTGATCTTAGGGGCAACATTTTCAACTTCTC 1364
 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 Db 1365 CCATTTGGTCTGGGAGGAGATGTCCTGAGGTCAATCTGCTACTTCTGGGAATGGCA 1424
 Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 Db 1425 ACATCTTCTGATCTCTTATTCAGTCTTCGACTTCAAGTGTGGGTCCACAGGACAG 1484
 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluArgAlaGlyLeuThrValPro 500
 Db 1485 ATATTGAAGGTTGTCACGCCAAAGTTAGCATGGAAGAGAGAGCCGCGCTCACTGTTCCTCA 1544

Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db 1545 AGGCACATAGCTTGTGTGTTCCACTTGCAGGATCGCGTTCATCTAAACTCCTT 1604

Qy 521 Ser 521
Db 1605 TCT 1607

RESULT 4

US-10-659-755-1
; Sequence 1, Application US/10659755
; Publication No. US20040128711A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: LIU, CHANG-JUN
; APPLICANT: DEAVOURS, BETTINA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
; TITLE OF INVENTION: AND ISOFLAVONOID NUTRACEUTICALS
; FILE REFERENCE: NBL:00705
; CURRENT APPLICATION NUMBER: US/10/659,755
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,447
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Soybean
US-10-659-755-1

Alignment Scores:

Pred. No.: 5,55e-317 Length: 1824
Score: 2250.00 Matches: 451
Percent Similarity: 86.56% Conservative: 0
Best Local Similarity: 86.56% Mismatches: 70
Query Match: 94.18% Indels: 0
DB: 18 Gaps: 0

US-09-857-581B-66 (1-521) x US-10-659-755-1 (1-1824)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db 54 ATGTTGCTGAACCTTGACCTGGTGTATTCGTTTGGCTCTGTTCTGCATTCGTCGCC 113
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAnProProSerPro***Pro 40
Db 114 ACACCCACTGCAAATCAAAAGCACTTCGCCATCTCCCAACCCCAAGCCCAAGCCT 173
Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
Db 174 CGTCTTCCTTCATAGACACCTTCATCTCTTAAAGACAAACTTCTCCACTACGCACCTC 233
Qy 61 IleAspLeuSerTysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db 234 ATCGACCTCTCCAAAAAATGATGGTCCCTTATTCCTCTCTACTTTGGCTCCATGCCAAC 293
Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db 294 GTTGTTCCTCCACACAGAAATGTTCAAGCTCTTCCTCCAAACGCAGAGCAACTTCC 353
Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db 354 TTCACACACAGGTTCCAAACCTCAGCCATAGAGCGCTCACCTNATGATAGTCNAGTGCC 413
Qy 121 *****Pro***GlyProTyrTrr***PheValArgLysLeuIleMetAsnAspLeu*** 140
Db 414 ATGGTTCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 473
Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db 474 AACGCCACCATGTGTAAACAAAGTTGAGGCGCTTTGAGGACCCCAACAGACCCCGCAAGTTCCTT 533

Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
Db 534 AGGTTATGCCCCAAGCGCAGAGCAGAGCCCTTGACTTGACCTGACCGAGGAGCTTCG 593
Qy 181 LysTrp***AenSerThr***SerMetMet***LeuGlyGluAlaGluGluLeuArgAsp 200
Db 594 AAATGGACCAACAGCAGCATCTCCATGATGATGCTCGCGAGGCTGAGGAGATCAGAGAC 653
Qy 201 IleAlaArgGluValLeuLysIle***GlyLysTyrSerLeuThrAspPheIle***Pro 220
Db 654 ATCGCTCGGAGGTTCTTAAGATCTTTGGCGAAATACAGCCTCCTGACTTTCATCTGGCCA 713
Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db 714 TTGAAGCATCTCAAGTTGGAAGTATGAGAAGAGGATCGACGACATCTTGAACAGTTC 773
Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArg***Asn 260
Db 774 GACCTGCTGTTGAAGGTCATCAAGAAGCGCGTGAGATCGTGAGGAGGAGAAAGAAC 833
Qy 261 GlyGlu***GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db 834 GGAGAGTTGTTGAGGTTGAGGTCAGCGGGGTTTCTTGACACTTTCCTTGAATTCGCT 893
Qy 281 GluAspGluThr***GluLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db 894 GAGATGAGACCATGGAGATCAAAATCACCAGGACCCATCGAGGGTCTTGTGTGCAC 953
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 954 TTTTCTCGCGAGCAACAGACTCCACAGCGGTGGCAACAGAGTGGGATTCGCGAGAACTC 1013
Qy 321 IleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLys 340
Db 1014 ATCAACCAATCCTAAGGTGTTGGAAAGCGCTCGTGAGGAGGTCTACAGTGTGTGGAAAG 1073
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCTTACATTAGAGCAATCGTGAAG 1133
Qy 361 GluThrPheArgMetHisProProLeuProValLysArgLysCys***GluGluCys 380
Db 1134 GAGACATTCGCGATGACCCGCCACTCCAGTGGTCAAAAGAAAGTGCACAGAGAGTGT 1193
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1194 GAGATTAAATGGATATGTGATCCCGAGGAGGACATTGATTTCTTCAATGTATGCCAAGTA 1253
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1254 GGAAGAGACCCCAATACTGGGACAGACCATCGAGTTCGTCCTGAGAGGTTCTTAGAG 1313
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1314 ACAGGGGCTGAAGGGGAGCAGGGCGCTTTGATCTTAGGGGACAAACATTTTCAACTTCTC 1373
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1374 CCATTGTTGGTCTGGGAGGAAATGTGCGCTCGGAGTCAATCTGGGCTACTTCGGGAATGGCA 1433
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db 1434 ACATCTTTCATCTCTTATTCAGTGTTCGACTTGCAGTGTGCGGTGCCACAGGACAG 1493
Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db 1494 ATATTGAAGGCTGCTGACGCCAAAGTTAGCATGGAAGAGAGAGCGCGCTCACCTGTTC 1553
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db 1554 AGGCACATAGCTTGTGTGTTCCACTTTGCAAGGATCGCGCTGTCATCTAAACTCCTT 1613


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; Sequence 3, Application US/10411225
; Publication No. US20040261146A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,225
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-225-3

Alignment Scores:
Pred. No.: 1,32e-126 Length: 1730
Score: 944.50 Matches: 198
Percent Similarity: 57.56% Conservative: 95
Best Local Similarity: 38.90% Mismatches: 189
Query Match: 39.54% Indels: 28
DB: 18 Gaps: 8

US-09-857-581b-66 (1-521) x US-10-411-225-3 (1-1730)
Qy 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro*** 39
Db 103 CCACCACCTTCCTCCTCCTCCTCGCGGA-AGGGACACCGTCTCGCGCGCTCCTC 161
Qy 40 ProArgLeuProPheLeGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla 59
Db 162 ---TCCCTACCCATAATGTCACCTCCACCTCCTCGGCCCAAGA---CTCCACCAACG 215
Qy 60 ***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetPro 79
Db 216 TTCATGAATTCACCTCAATACGGCCCAATTGATCCAGCTCAAGCTCGGCTCGATCCCG 275
Qy 80 ThrValValAlaSerThrProGluLeuPheLysLeuLeuGln*****GluAlaThr 99
Db 276 TGCCTCTGCGCTCGACCGCGAGCTCGGAGAGATTCTTAAGACGACGAG---CTC 332
Qy 100 SerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****Val 119
Db 333 CGGTTCTCCTCGCGAAGCACTCTACGCCCATAGACATCGTCACTACGACTCGTCTCTT 392
Qy 120 Ala*****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu 139
Db 393 GCCTTCTCTCGTACGACCGCTCTGGAAGTACATCAAGAACTGTGTACTCTACGAGCTG 452
Qy 140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
Db 453 CTCGAGCGAGGAACCTCGACACATTTTCAGCCCATTAGGAATCTCGAGGTCAGTCTCTT 512
Qy 160 LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
Db 513 CTCGAGCTTCTGATGCAAGAGCTTTAAGGGCGAGAGTGTGAATGTGACAGACGAGCTG 572

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Qy 180 LeuLysTrp***AsnSerThr***SerMetMet***Leu----- 192
Db 573 GTGAGGCTACGACGAATGTGATATCCACATGATGCTGAGCATAGGTCCTCGGAAGAT 632
Qy 193 ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGlu 211
Db 633 GAAGGCGATGCTGAGCGCGCGAGAACAGTCATACGCGAGGTGACGAGATATTTGGGAA 692
Qy 212 TyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLys 231
Db 693 TTCGATGTTACGACATATATGCTTTTGCAGAAATTCGATCTCGAGGGGATAAAGAG 752
Qy 232 ArgIleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArg 251
Db 753 AGGTTCAGAGGATATTCAGAGGAGGTATGATGCTTTGTCGAGAGAGATATTAGTAGATA 812
Qy 252 Arg***IleValArgArgArg***AsnGlyGlu*****GluGly-----Glu*** 268
Db 813 GAGAGA-----TCGAGGAGGCAAAATCGTATAAGCATGGTGGCGGTAAACATAGGAG 866
Qy 269 SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLys 288
Db 867 GCCAAGGATTTCTTCATATGTTGCTTGTGATGTCATGAGAGTGGGACACGAGGTCAA 926
Qy 289 IleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSer 308
Db 927 TTCCTAGAGAGCATCTCAAGGCTTTGATTTCTGATTTCTTTCACGGCGGTACGGACACA 986
Qy 309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
Db 987 ACAGCCATAGCCACCGAGTGGGCCATCGCGAGCTCATCAACAACCGACGCTTTGAAG 1046
Qy 329 ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
Db 1047 AAGGCCCAAGAGAAATATATCCCGGATCATCGGACCAACGCGATCGTACAAAGATCCGAC 1106
Qy 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
Db 1107 GCCCAGACCTACCTACCTCCAGGCCATCATCAGAGACGTTCCGGCTCCACCCACCG 1166
Qy 369 LeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
Db 1167 ATCCCGATGCTCTCGGTAAGTCCACCTCGGATTCGAGGTCAACGGCTACAAATCCAA 1226
Qy 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
Db 1227 GCCAAGAGCTCTTGTTCGTGAACATATGTCATCGGTCCGAAACCTTAATTAACGGAA 1286
Qy 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
Db 1287 AGCCCTATGAGTTTCAGGCCCGGAGCGGTTCTTGAGAGAGGAGCGCGAG----- 1334
Qy 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
Db 1335 TCCATCGAGCTCAAGGCCGACACTTTGAGCTCTTGCCTTTTGGGAGCGGCGCAGGGC 1394
Qy 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
Db 1395 TGTCCCGGATGTTGTCGTATACAGAGGTGTCAGCATCATTCATTCGGACCATGGTTCAG 1454
Qy 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
Db 1455 TCGTTTCAC-----TGGAAATTCGACATGGTTCGGGCAATAAT 1493
Qy 489 ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
Db 1494 GTGACATGACCAACCGTCTGGATTGACCGCTCCGAGAGCGTTCGATCTCTGTTGCCGG 1553
Qy 509 ProLeuAlaArgIleGlyValAlaSer 517
Db 1554 TTGATTCACGGGTTGCCCGGCCACA 1580

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RESULT 8

US-10-411-115-1
 ; Sequence 1, Application US/10411115
 ; Publication No. US20040003431A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako
 ; APPLICANT: Kasumi, Takaaki
 ; APPLICANT: Ayabe, Shin-ichi
 ; APPLICANT: Akashi, Tomoyoshi
 ; TITLE OF INVENTION: Genes Coding for Flavone Synthases
 ; FILE REFERENCE: 001560-383
 ; CURRENT APPLICATION NUMBER: US/10/411.115
 ; CURRENT FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US/09/672,785
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
 ; PRIOR FILING DATE: 2000-01-30
 ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: JP 11-205229
 ; PRIOR FILING DATE: 1999-01-19
 ; PRIOR APPLICATION NUMBER: JP 11-22427
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1724
 ; TYPE: DNA
 ; ORGANISM: Antirrhinum majus
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
 ; OTHER INFORMATION: activity to directly convert flavanone to flavone
 US-10-411-115-1

Alignment Scores:

Pred. No.: 1.84e-126 Length: 1724
 Score: 943.50 Matches: 198
 Percent Similarity: 57.31% Conservative: 88
 Best Local Similarity: 39.68% Mismatches: 179
 Query Match: 39.49% Indels: 34
 DB: 17 Gaps: 9

US-09-857-581B-66 (1-521) x US-10-411-115-1 (1-1724)

Qy 33 ProAsnProProSerPro***Pro-Arg-*****LeuPr 43
 Db 87 CCTCACCCCTCTAAACCGCACCCGCGCAAGACCGCGCCGCCCATTTAGCCCTCCC 146
 Qy 43 oPheileGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLe 63
 Db 147 CTTAATAGGCACATTACACCTCTCTGGGCCCAAG---CTCCACACACCTTCCACCAATT 203
 Qy 63 uSerLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 83
 Db 204 CTCCCAACCGCTACGCGCGCTCATCCAGCTCTACCTCGGCTCCGTCGCTCGTCCG 263
 Qy 83 aSerThrProGluLeuPheLysLeuLeuGln*****GluAlaThrSerPhe***Th 103
 Db 264 TTCCACGCGCGCAATTCCTCAAGACGCAAGAA---CTCGACTTCTCGTC 320
 Qy 103 rArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla*****Pr 123
 Db 321 CCGCAAGCACTCCACCGCCATCGACATCGTCAGCTCCTCGTTCGCTTCGCGCC 380
 Qy 123 o***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaTh 143
 Db 381 GTACGCGCGCTACTGGAATTCATCAAGAAATTATGACTTACGAGCTACTGCGTCCG 440
 Qy 143 rThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Me 163
 Db 441 GAACCTGAGCCATTTCCAGCCCATTTAGAGCTTTTGAGGTCAACAGTTTCTTTGAGAATTT 500
 Qy 163 tAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp** 183

Db 501 GTACGAGAAACACAGCAGAGAAACACAGAGTGTAAATGTGACTGAGGAGCTTGTGAAGCTGAC 560
 Qy 183 *AsnSerThr***SerMetMet***Leu-*****GlyGluAl 195
 Db 561 GAGTAATGTGATCAGTAACATGATGTTGGGATCAGGTGTCGGGGACGGAAGGGAGGC 620
 Qy 195 aGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuTh 215
 Db 621 GGAGTGGCGAGGACGGTGATAGGGAGGTGACCCAGATATTTGGGAGTTGATGTC 680
 Qy 215 rAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAs 235
 Db 681 GGAGATTGTTGTTGTTAAGAAATTTGGATCTCGAGGGGATTAGGAAGAGTCCGAGGA 740
 Qy 235 pIleLeuAsnLysPheAspProValValGluArgValIleLysLysArg***IleVa 255
 Db 741 TATTAGGAGGAGGTATGATGCTTTGTTGGAGAAATATTAGTATAGGGAGAGGTTG-- 798
 Qy 255 lAtgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspTh 275
 Db 799 -AGTTGAGGGGGGGTGGTGGTGGAGGGGTGGAGAGGTGAAGGAT---TTTTTGGATAT 854
 Qy 275 rLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile** 295
 Db 855 GTTGTGGATGTGATGAGAGTGAAGAAATCGAGGTGGAGTTTACGAGGGAGCATCTCAA 914
 Qy 295 *GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTr 315
 Db 915 AGCTTTGATTTGGAATTTCTTCACTGCGGTGACAGACACACACCAATTCACACAGAAATG 974
 Qy 315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
 Db 975 GGCATAGCAGAACTCATTTAGCAATCCAAATGTTACTCAAAAAGCTCAAGAGAGATGGA 1034
 Qy 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
 Db 1035 CAAAGTCATAGGATCAACAAAGTTGTTGCAAGATCCGACGCCCTAACTTGCCTTACCT 1094
 Qy 355 eArgAlaIleValLysGluThrPheArgMetHisProLeuProValValLysArgLys 375
 Db 1095 CAACGCGATCATAAAGAAACGTTCCGCTCCACCCCTCCAAATCCCATGCTCACTAGAAA 1154
 Qy 375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
 Db 1155 ATCAATTTCTGACGTTGTTGTTCAACGGGTACACGATCCCTGCCAAAACGCTATTGTTGT 1214
 Qy 395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
 Db 1215 CAACCTTTGGTCCATCGGAAGGAATCTTAATCTACTGGGAAATCCGATGGAGTTCCGACC 1274
 Qy 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
 Db 1275 CGAGAGGTTTCTCGAGAAAGGG-----ACCGGGTCTGATAGACGTTAAAGGGCA 1322
 Qy 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
 Db 1323 GCATTTTCAGTTGCTCGCTTTGGCAGCGGCGGGGGCTCCCGGGGATGTTGTTAGG 1382
 Qy 455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 475
 Db 1383 CATGACGAGTTGTTTAGTATTATCGGGGCTATGTCAGTGTTCGATTCGATAAATG-- 1440
 Qy 475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
 Db 1441 ----CCCGATGGTGTG-----AAGTCGTCGATCATGACCGAGCGGCC 1478
 Qy 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
 Db 1479 CGGTTGACGCTCCAGTCCCAATGATTTGGTGTGCAATTTGTTGCCACGGATT 1533
 RESULT 9
 US-10-411-225-1

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; Sequence 1, Application US/10411225
; Publication No. US20040261146A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,225
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1:
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-225-1

Alignment Scores:
Pred. No.: 1.84e-126 Length: 1724
Score: 943.50 Matches: 198
Percent Similarity: 57.31% Conservative: 88
Best Local Similarity: 39.68% Mismatches: 179
Query Match: 39.49% Indels: 34
DB: 18 Gaps: 9

US-09-857-581b-66 (1-521) x US-10-411-225-1 (1-1724)
Qy 33 ProAsnProProSerPro***Pro-Arg-----LeuPr 43
Db 87 CCTCACCTCTTAAACCGCAGCCGCGCGAGACCGCGCCGCCGCGCCATAGCCCTCC 146
Qy 43 oPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLe 63
Db 147 CTTAATAGGCGCACTTACACCTCTCTCGGCCCAAG---CTCCACCAACACCTTCCACCAATT 203
Qy 63 uSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 83
Db 204 CTCCCAACGCTACGCGCGCGCTCATCGAGCTCTACCTCGGCTCGCTCCGTCATGCGTGC 263
Qy 83 aSerThrProGluLeuPheLysLeuLeuGln*****GluAlaThrSerPhe***Th 103
Db 264 TTCCACGCGCGCACTCGCGCGCAATTCTCTCAAGACGACGAA---CTCGACTCTCGTC 320
Qy 103 rArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla*****Pr 123
Db 321 CCGCAAGCACTCCACCGCCCATGACATCGTCAGTACGACTCTCTCGTTCGCTTCGCGCC 380
Qy 123 o***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaTh 143
Db 381 GTACGCGCGCGTACTGGAAATTCACAGAAATATGATCTTACGAGCTACTGGGTGCCG 440
Qy 143 rThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Me 163
Db 441 GAACCTTGAGCCATTTCACGCGCCATTAGAGCTTTGGAGGTCAACAGTTTCTTGAGATT 500
Qy 163 tAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp** 183
Db 501 GTACGAGAAACACAGACAGAAACAGAGTGTGTAATGTGACTGAGAGCTGTGTAAGCTGAC 560
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RESULT 10

US-10-411-115-7

; Sequence 7, Application US/10411115

; Publication No. US20040003431A1

GENERAL INFORMATION:
 APPLICANT: Mizutani, Masako
 APPLICANT: Kasumi, Takaaki
 APPLICANT: Ayabe, Shin-ichi
 APPLICANT: Akashi, Tomoyoshi
 TITLE OF INVENTION: Genes Coding for Flavone Synthases
 FILE REFERENCE: 001560-383
 CURRENT APPLICATION NUMBER: US/10/411,115
 CURRENT FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: US/09/672,785
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: PCT/JP00/04379
 PRIOR FILING DATE: 2000-01-30
 PRIOR APPLICATION NUMBER: PCT/JP00/00490
 PRIOR FILING DATE: 1999-01-28
 PRIOR APPLICATION NUMBER: JP 11-205229
 PRIOR FILING DATE: 1999-01-19
 PRIOR APPLICATION NUMBER: JP 11-22427
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 7

LENGTH: 1770
 TYPE: DNA
 ORGANISM: *Perilla frutescens*
 FEATURE:

OTHER INFORMATION: Nucleotide sequence encoding a protein having an activity to directly convert flavanone to flavone
 US-10-411-115-7

Alignment Scores:
 Pred. No.: 3,13e-123 Length: 1770
 Score: 921.50 Matches: 190
 Percent Similarity: 57.46% Conservative: 91
 Best Local Similarity: 38.85% Mismatches: 183
 Query Match: 38.57% Indels: 25
 DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-411-115-7 (1-1770)

Qy 33 ProAsnProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
 Db 99 CCTTACCTCCCGGCGGCTTCCCT---CTTCCCATCATCGGCCCATACCTCTCTCGGG 155
 Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLysPheSer 72
 Db 156 CCGAGA---CTCCACCAACCTTCACAGATCTGCCAACGGTAGCGGCCCTTAATGCAG 212
 Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
 Db 213 CTCCGCTCGGGTCCATCCGCTGCTCATCTGCTCGCGGAGCTCGCCCAAGAAATGC 272
 Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
 Db 273 CTCAAGACACACGAGCTGCTC---TTCTCTCCCGCAACACTCCACCGCCATTTGATATC 329
 Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg 132
 Db 330 GTCACTACGATTCATCTCTCTCTCCCTACGGGCGCTTCTGGAATTCATCAAG 389
 Qy 133 LysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg 152
 Db 390 AAATATGACCTACGAGCTGCTCGGGCCCGGAATCTCGCCCATTTTCAGCCCATCAGG 449
 Qy 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
 Db 450 ACTCTCGAAGTCAAGTCTTCTCTCCAAATCTTATGCGCAAGGGTGAATCGGGGAGAGC 509
 Qy 173 LeuAsp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu 192
 Db 510 TTCAACGTGACTGAGGAGCTCGTGAAGCTGACGAGCAACGTCATATCGCATATGATGCTG 569
 Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204

Db 570 AGCATACGGTGTTCAGACGCGAGTTCGAGCGCGAGCGCGGAGCGTATTTCGGGAG 629
 Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
 Db 630 GTACGCGAGATATTGGGGAGTTCGACGTCTCCGACATCATATGCGTCTTGAAGACATTC 689
 Qy 225 LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal 244
 Db 690 GATTTCCAAGGTATAAGGAAGCGTCCGAGATATCCAGAGGAGATATGATGCTCTGCTG 749
 Qy 245 GluArgValIleLysLysArgArg***IleValArgArg***AsnGlyLys*** 264
 Db 750 GAGAAGATCATCCGACAGAGAGAAG-----CAGAGGCGGACCCAGCGGGCGGTGGC 803
 Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284
 Db 804 GCGCGCGGGAAGCCAGGATTTCTTGACATGTTCTCGACATAATCGAGAGCGGGA 863
 Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304
 Db 864 GCGAAGTTAAATTCAGGAGGAGCATCTCAAAGCTTTGATTTCTGGATTTCTTCCAGCC 923
 Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuAsnAsnPro 324
 Db 924 GGCACCGACACGCGCGGATCGTGTGTAATGGCGGATAGCAGAGTGATCAACAATCCA 983
 Qy 325 ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal 344
 Db 984 AATGTGTGAAGAAAGCTCAAGAGAGATGTCGAACATCTCGGATTCGACAGATTCG 1043
 Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
 Db 1044 CAAGAATCCGAGCGCCCAATCTGCTTCAAGCCCTCATCAAGAAACATTTCCGG 1103
 Qy 365 MethHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
 Db 1104 CTCCACCTCCAAATCCCAATGCTCGCGAGGAAATCGATCTCGGACTGCTGATCGACGC 1163
 Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404
 Db 1164 TACATGATTCGGCCACACGCTGCTCTTCTGTCACCTCTGTCATGCGGCGGACCT 1223
 Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
 Db 1224 AAATCTGGGACTACCCGACGCGCTTCAGCGGAGAGGTTTCTGGAGAAG----- 1274
 Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
 Db 1275 ---GAAAGGCGCGCATCGATGTTAAAGGGCAGCATTTTGAGCTGTACCGTTCGGAACG 1331
 Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
 Db 1332 GCGAGGAGAGCTCCCGAGGATGCTTTAGCCATTCAGGAGGTGGTTCATCATTAATGGG 1391
 Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
 Db 1392 ACGATGATTCATCTTCGATTGGAAGCTG-----CCCGACGCG----- 1430
 Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
 Db 1431 ---TCCGCCATGTTGATATGCGAGAACCGCGGCTCAGCGCACCGCGAGAGCCGAT 1487
 Qy 505 LeuValCysValProLeuAlaArgIle 513
 Db 1488 TTGTTTTCGCGTGGTGGCGCGAGTT 1514

RESULT 11

US-10-411-225-7
 ; Sequence 7, Application US/10411225
 ; Publication No. US20040261146A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako

Qy	259	***AsnGlyGlu*****GluGlyGlu***SerClyVal***LeuAspThrLeuLeuGlu	278
Db	850	AAG-----GAGAGAGGGAGGGAGGAGATTAGGATTGCTAGATATTGTTGGAA	903
Qy	279	PheAlaGluAspGluThr***GluLeuLeuGlyLeuThrLys*****Ile***GlyLeuVal	298
Db	904	ATTTCATCAAGATGAGCAGGGAGATCAAGTTATCTAGAGAGAATGTCAGAGGCTTTTCATC	963

[illegible]

1024	GGATTAAATCAACAACCAACCAICATGATGGAGAAAGGCAAGACACAGAGATAGAGATTTCAGTGACA	
Qy	GlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIle	358
Db	GGGAAACAAAAGGGCTAATACAAGAATCAGATCTTTCCCAACCTTCATCACTCTACAAAGCCATA	1143
Qy	ValLysGluThrPheArgMetHisProLeuProValValLysArgLysCys**Glu	378

DD 1144 GTCATAGAGAAACACCTAAGGATTCAACCCCTACAGCGCCAC TGC TAGGGAGAGAGAA TCA TCAGAA 1205

QY 379 Glucy s... ::: :||| PQQGUGUYAADAU.....PNEASHVALIIP 398
Db 1204 AGCTGCAATGATGTGGCTATGCACATTCCAGCAAAGTCCTTAGTGTTTGTTAATCTGTGG 1263

Cy		399	Glnvaltyr--ASP---	LYSLYLIPASPARGLPISERGLR--	AAGPIGIDUALSPLE	418
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	:	:	:	:	:	:
D6		1264	TCTATGGGAAGGCACCCAAAATT	TTGGGAGGACCCTTCTTGAGTTCAAGCCAGAGAGTTT	1323	

D_b
1324 ATGAAC-----AATATGAAGACAACAAATTGATGTAGGGGCAGAAATTTCCAG 1374
||||| Leu::Leu::Gly::-::His::Met::
419 LeuGluuuu---AagaAcGyYuuu- Leu::Leu::Gly::-::His::Met::
C_T

1375 CTATTGCCATTGGGCACTGGGAGAAAGGTGTGCCCTGGTGCATCCTTGCATCTTCAGACT 1434

Db
1435 GTGCCTACTAAGCTTGCTGCTATGATTCAGATGCTTTGAATTAGGGTT-----1482

Db 1483 -----GATGGGACTGTTAGCATGGAGAAAAACCAAGCATGACA 1521

Db 1522 CTTCTAGGGCACATCTTTGATTTGTCTCTGTGCCACGCATGAACCTT 1572

US-10-424-599-78567
; Sequence 78567, Application US/10424599
; Publication No. US20040031072A1
; CERNET, INFORMATION

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yanna
APPLICANT:

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? CURRENT FILLING DATE: 2003-04-28
? NUMBER OF SEQ ID NOS: 285684
? SEQ ID NO 78567
? LENGTH: 3128
?

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1 TYPE: DNA
2 ORGANISM: Glycine max
3 FEATURE:
4 OTHER INFORMATION: Clone ID: PAT MRT3847 41962C.1
5

RESULT 13

US-10-424-599-78567

; Sequence 78567, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28

; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEC ID NOS: 285684

; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 79557

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; SEQ ID NO 78567
;
; LENGTH: 3328

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; LENGTH: 3328
: TYPE: DNA

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TYPE: DNA
ORGANISM: Glycine max

ORGANISM: *GLYCYMME MAX*
FEATURE:

FEATURE: OTHER INFORMATION: Clone ID: PAT MRT3847 41962C.1

OTHER INFORMATION: CLORE ID: FBI_MK13847_41902C.1

US-10-424-599-78567

Alignment Scores:

Pred. No.: 2,15e-116 Length: 3328
Score: 877.50 Matches: 188
Percent Similarity: 57.03% Conservative: 92
Best Local Similarity: 38.29% Mismatches: 183
Query Match: 36.73% Indels: 28
DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-424-599-78567 (1-3328)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 176 CCACCAAGTCA---AAGGCCCTTCCATAATTGGCCACCTCCACCTTGG---TCCCCA 229
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
DB 230 ATTCACCCACCAAGATTTTACAAGCTCTCAACCGCCGACGAGCCCATCATGCAACTTTTC 289
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheGln 94
DB 290 CTTGGCTCAGTCCCTGTGTGGCTTCCACCGCAGAACGCCCAAGAGTTTCCTTAA 349
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 350 ACCCAGAAATCAACTTCTCAACCGCCGCGCCAAACGTCGCGTTAAGGGCTTAGCC 409
QY 115 TyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheVal 131
DB 410 TAGGATTCACCAAGACTTCTTTTGGCGTTTGCACCTTTCGGACCTTACTGGAAGTTTCATG 469
QY 132 ArgLysLeuLeuMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeu 151
DB 470 AAGAAACTCTGCATCTCCGAGCTTCTCAGCGCGCGAATGATGACCACTTCTTCCCGTG 529
QY 152 ArgThr-GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***Ly 171
DB 530 AGGTACAGACAGACCAAGAGATTCATCAGCGCGGTGTTCCGAAAGAGTTCGCGCGCA 589
QY 171 sProLeuAsp***ThrGluGluLeuLysTrp***AsnSerThr***SerMetMet** 191
DB 590 GGCGGTGGATTCGAGACAGAGCTCATGACACTCTCCAAACAACATCGTATCCAGAAATGAC 649
QY 191 *Leu-----GlyGluAlaGluLeuIleArgAspIleAlaAr 203
DB 650 GCTGAGTCAGAAAGACTTCTGAGACGACAAACAGGCTGAGGAGATGAAGAGTCTGTC 709
QY 203 gGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys** 223
DB 710 GAATATCGCGAGCTCATGCGGAGTTCAAGTTTCGACTTCTATTGTTGTTACTGAGCC 769
QY 223 *LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVa 243
DB 770 TTTGATTTGCGGGTTCAACAGAAAATCAAGGAGACTCGGACAGAGTTTGACGTGT 829
QY 243 lValGluArgValIleLysLysArgArg***IleValArgArg***AsnGlyGlu** 263
DB 830 GGTGCGGAATCAATAAGCAGCGCTCAAGAG-----GAAAGAGGAAGAAACAAAGAAC 883
QY 263 ***GluGlyGlu***SerGlyVal***LeuAspThrLeuGluPheAlaGluAspG1 283
DB 884 GGGCAGACGAGCTCAGTTTAAGGATATGCTTGATGTTTATTCGACATAGCGAGATGA 943
QY 283 uThr***GluLeuLysIleThrLys*****Ile***GlyLeuValValAsp***PheSe 303
DB 944 CAGTCTCTGAATCAATTAACCAAGAAAACATTAAGCGCTTCATCATCATGATATTTGT 1003
QY 303 rAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsnAs 323
DB 1004 TGCGGGAGCTGACACGCTGCAACCATGGAATGGGCTTATGCGAGAGTTATCAACAA 1063
QY 323 nPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***Le 343

DB 1064 TCCATATGTGTGGAGAGGCAAGCATAGATAGATCGGTGTTGGAAAAGTAGAAT 1123
QY 343 uValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPh 363
DB 1124 GGTAGAAGAATCAGATATTGCCAACCTTCTTACTTTGCAAGCCATTGTTAGAGAAACACT 1183
QY 363 eArgMetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAs 383
DB 1184 TAGGCTTCAACCCAGGTGTCATTTGTTTAGAATCATCAAAAGTGCAGGTGTTG 1243
QY 383 nGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***As 403
DB 1244 TGGGTATGATATTCACGACAAAGACTCGATTATTGTCAATGTTTGGCTATTTCGTAGGA 1303
QY 403 p***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***Al 423
DB 1304 TCCCAATCATCTGGGAGAAACCTTTTGAAGTTTAGCCAGAGAGTTTATCAGA----- 1355
QY 423 aGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheG1 443
DB 1356 -GATGGCAA---AATCAATTTGATGTTAGGGGCAACATTAATTTATTCATTCGG 1411
QY 443 ySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLe 463
DB 1412 GAGTGAAGAAGAACCTGCTGCTTCTCTAGCGTGCAGGTTGTGCTGTGAATCT 1471
QY 463 uAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLy 483
DB 1472 GGCTATAATTAATTCATATGTTTCCATGGAAGCTTGTGTGGCAATGGC----- 1520
QY 483 sGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHi 503
DB 1521 -----AAGTGACATGGAAGAAGCTGTGGATCCTCTCTCCGAGGGCTAA 1567
QY 503 sSerLeuValCysValProLeuAlaArgIle 513
DB 1568 CCCATAATTGTGTCCCTGTTTCCAAAGATT 1598

RESULT 14

US-10-424-599-120588
; Sequence 120588, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120588
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7989C.1
US-10-424-599-120588

Alignment Scores:
Pred. No.: 1,1e-115 Length: 1842
Score: 870.00 Matches: 189
Percent Similarity: 55.42% Conservative: 82
Best Local Similarity: 38.65% Mismatches: 192
Query Match: 36.42% Indels: 26
DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-424-599-120588 (1-1842)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54

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Db 302 CACCGAGTCCAAATGCC---CTACCCATCATGTGACACCTCCACCTTCTT---TCTCCA 355
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerIysLysHisGlyProGluLeuPheSer***** 74
Db 356 ACACCTCACCAAGATTTTCCACAGCTCTCCTCCGCTATGACCCATATACACCTTTT 415
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 416 CTGTGTTCCAGTCCCTCGTGTGGTCTCCACAGCAGAGCGCGCAAGAGTTCCTCAA 475
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 476 ACTCAAGAACCGCGCTTCTCCAACCGCCCGCTAACTGTGCGCGTCCGAACCTTAACC 535
Qy 115 Tyr---Asp*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 536 TAGCGGTCCGAAGACTTCTGTTCGCACCTTACGACCCCTATTGGAAGTTTATGAAGAA 595
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 596 CTCTGCATGTCCGAATCTCTCGGTGGCCACATGCTGGACCAAGTTTCTTCCCGTGAGACAG 655
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 656 CAAGAGACAAATAATTCATCAACCGTGTCTCCAAAGGGTATTCTGTGTGAGCGCGTG 715
Qy 174 Asp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu--- 192
Db 716 GATTTGGGGAGAGTTTCATACGCTTCGAACAACATCGTGTGAGAAATGATCGTAGT 775
Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204
Db 776 CAGACGAGTACTACTAGGACGAGAACGAAGTTGAAGAGATCAGGAAGCTGTGAAGAT 835
Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 836 GCCGACAGAGCTCTCGGGAAGTTCAACATATCGGACTTCGTTCGTTCTTGAAGCGCTTT 895
Qy 225 LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal 244
Db 896 GATTTGACGGGTTCACAGAGGCTCGAAGATTCGGGACTGCTTTGACACCGTGTG 955
Qy 245 GluArgValIleLysLysArgArg***IleValArgArg***AsnGlyGlu***** 264
Db 956 GACAGATCATAAACCAACGTTGAAG---GAAAGAGCAACAGATGAACCGTTGGA 1012
Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284
Db 1013 AAACGAGAAATTAAGGATATG---CTTCATGTTTGTGTTGACATATCTGAAGATGAGAT 1069
Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValasp***PheSerAla 304
Db 1070 TCTGAATTAATTAACAAAGAAACATTAAGGCCAATATCTTGGACATATTAAATGCT 1129
Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
Db 1130 GGGACTGACACCTCAGCTGTACGATGAATGGGCTATGGCAGAGTTAATCAACAATCCA 1189
Qy 325 ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal 344
Db 1190 GGTGTGTGGAGAGGCAAGCAAGAAATGATGTCAGTGTGTGGAAGAGTAGTAATAGTA 1249
Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
Db 1250 GAAAGATCAGATATGTCACACCTCTCTTACTTTGCAAGGCATTTGTAGAGAACAATTAAGA 1309
Qy 365 MethisProProLeuProValLysArgLysCys***GluGluCys***IleAsnGly 384
Db 1310 CTTACCCAGCTGGTGCATTCGTTTATAGAGATCATAGAGAGCTGTGCTGTGTGGG 1369
Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404
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Db 1370 TATGATATTCCAGCAAGACTCGATTATTGTCAATGTTTGGGCTATTGGTAGGACCCC 1429
Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
Db 1430 AATCACTGGGAGAACCTCTTCTGAGTTTAGGCAGAGAGTTTGTGAAATGGG----- 1483
Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
Db 1484 -----AAGAGTCAATTGGATGTTAGGGGCAACATATCATCTACTTCCGTTCCGTAGT 1537
Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
Db 1538 GGAAGAAGAGCATGCTCTGGTACTTCTTGGCATTTGCAAGTTGTGCATGTGCAATTTGCA 1597
Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
Db 1598 GTTCTAATTCAGTGTGTTCATGAAGTTGACTGTGCAATGGC----- 1642
Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
Db 1643 -----AAGGTGAACATGGAAGAAAGGCTGGCATCACTCTTCCGAGGGCTCACCCC 1693
Qy 505 LeuValCysValProLeuAlaArgIle 513
Db 1694 ATAATTTGTGTCCTATTTCGAAGACTT 1720

RESULT 15
US-10-424-599-101968
; Sequence 101968, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 101968
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1906)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63093C.1
US-10-424-599-101968

Alignment Scores:
Pred. No.: 1,02e-111 Length: 1906
Score: 843.00 Matches: 185
Percent Similarity: 55.24% Conservative: 84
Best Local Similarity: 37.99% Mismatches: 190
Query Match: 35.29% Indels: 28
DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-424-599-101968 (1-1906)

Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 200 CCACCGAGTCCA---AAGGGCCCTTCCCATATTGGGACCTTCCACCTTTGTG---TCCCCA 253
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 254 ATACCCCAACCAAGATTTTACAGCTCTCACTCGCCATGAGCCCATCATGCAACTTTTC 313
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
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Qy 95 *****GluAlaThrSerPhe*****ThrArgPheGlnThrSerAla*****Arg*****LeuThr 114
Db 374 ACCCAGCAATCAACTTCTCCACCGCCCGCGCAAAACGTCGCGTTCAGTTCCTTAACC 433
Qy 115 TyrAsp*****ValAla*****Pro*****GlyProTyrTrp*****PheValArgLysLeu 134
Db 434 TAC-----GTGTTTGGCCCTTACGGACCCCTCCGTGAAGTTCATCAAGAACTT 481
Qy 135 IleMetAsnAspLeu*****AsnAlaThrThrValAsn*****LeuArgProLeuArgThrGln 154
Db 482 TGCATGTCCGAACCTCTCGGTGGCGCATGTCGACCACTTCCTCTGTGAGACAGCAA 541
Qy 155 GlnIleArgLys*****LeuArg*****MetAlaGln*****AlaGluAla*****LysProLeuAsp 174
Db 542 GAGACAAAATAATTCATAACACGCTCTCCAAAGGGTATCGTGTGTAAGCCGTTGAC 601
Qy 175 ***ThrGluGluLeuLysTrp***AsnSerThr***SerMetMet***LeuGly--- 193
Db 602 TTCGGAGGAGGTTTCATGAGACTCTCCAAACATCATTTTCGAGATGACCATGAACCAG 661
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeu 206
Db 662 ACGAGTTCCGAGGACGAGAAACAGCGCCGAAAGATGAGGATGCTGTGGCGGATGTCGCA 721
Qy 207 LysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysVal 226
Db 722 GAACATCATGGCAGGTTCAACGTGTCGAGCTTCATTTGGTCTTGAAGCCTTTTGATTG 781
Qy 227 GlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValValGluArg 246
Db 782 CAGGGTTCAACAGAGGATCAGGAAACAGGAGTATCGACGCTGTCTTGGACAGA 841
Qy 247 ValIleLysLysArgArg***IleValArgArg***AsnGlyGlu*****GluGly 266
Db 842 ATCATCAAGCAGCGCTGAAGAG-----GAAAGAAGGAAACAACAAGGAAATCGGTGGAACG 895
Qy 267 Glu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***Glu 286
Db 896 CGTCAGTTTAAGGATATACTTGTGTTTGTGGACATAGCGGAAGATGACAGTCTCGAA 955
Qy 287 IleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly*** 306
Db 956 ATCAATTAACCAAGAGACATTAAGCGCTTCATCATGATATATTTGTTCGCGGACT 1015
Qy 307 AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsnAsnPro***Val 326
Db 1016 GACACGTGAGTCAACCATGGAATGGGCTATGGCAGAGTTAATCAACAATCCATGTTGTG 1075
Qy 327 Leu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGlu 346
Db 1076 TTGGAGAAGGCAAGCAAGAGATAGATGTCAGTGGTTGGAAATAGTAGAATAATAGAGAA 1135
Qy 347 ValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMethHis 366
Db 1136 TCAGACATGTCACCTTCTTACCTACAGCCATTGTTAGAGAAACACATTAGGATTCAC 1195
Qy 367 ProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val 386
Db 1196 CCAGGTGGTCCATTGATTGTAGAGATCATCAAAAAGTGTGTGTTTGTGGGTATGAA 1255
Qy 387 ***ProGluGlyAlaLeu*****PheAsnValTyrGlnValGly***Asp***LysTyr 406
Db 1256 ATTCACCGCAAGCCCATTTTGTCAATGTTTGGGCTATTGGAAGGGACCCCAATCAT 1315
Qy 407 TrpAspArgProSerGlu*****ArgProGluArgPheLeuGluThr*****AlaGluGlyGlu 426
Db 1316 TGGGAGAACCCATTGAGTTTAGCCCGGAGAGGTTTTTTTGAA-----AATGGACAA 1366
Qy 427 Ala*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg 446
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Qy 447 ***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeu 466
Db 1424 AGATCATGCGCTGGTACTTCTCTGGCATTTGCAGATTGTGCATGTGAATCTGGCTATTATG 1483
Qy 467 IleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***Asp 486
Db 1484 ATTCAGTGTGTTTTCAGTGAAG-----TTTGATAATGGCAAT 1519
Qy 487 AlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuVal 506
Db 1520 AACAAAGTGGACATGGAAGAAGTCTGCGATCCTCTTCGAGGGCTCACCCATAATT 1579
Qy 507 CysValProLeuAlaArgIle 513
Db 1580 TGTCCTCTGTTCCAAAGCTT 1600
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Search completed: April 29, 2005, 19:35:37
Job time : 913 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2005, 17:20:49 ; Search time 82 Seconds
(without alignments)
2116.443 Million cell updates/sec

Title: US-09-857-581B-66

Perfect score: 2389

Sequence: 1 MLLELALGLXVLALFXHLRP.....AHSLVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	94.4	521	15	US-10-310-154-735 Sequence 735, App
2	2250	94.2	521	16	US-10-659-755-2 Sequence 2, Appli
3	944.5	39.5	512	15	US-10-411-115-4 Sequence 4, Appli
4	940.5	39.4	506	15	US-10-411-115-2 Sequence 2, Appli
5	921.5	38.6	506	15	US-10-411-115-8 Sequence 8, Appli
6	919.5	38.5	509	15	US-10-424-599-149724 Sequence 149724,
7	891.5	37.3	509	15	US-10-424-599-221409 Sequence 221409,
8	870	36.4	510	15	US-10-424-599-263430 Sequence 263430,
9	843	35.3	502	15	US-10-424-599-244810 Sequence 244810,
10	807.5	33.8	579	16	US-10-437-963-150757 Sequence 150757,
11	761.5	31.9	518	16	US-10-437-963-123495 Sequence 123495,
12	730.5	30.6	516	16	US-10-437-963-169616 Sequence 169616,
13	717	30.0	513	15	US-10-424-599-243352 Sequence 243352,

14	701.5	29.4	509	15	US-10-424-599-258259 Sequence 258259, A
15	691.5	28.9	548	15	US-10-425-114-64368 Sequence 64368, A
16	657	27.5	540	16	US-10-437-963-140857 Sequence 140857,
17	651	27.2	509	14	US-10-097-559-11 Sequence 11, Appl
18	649.5	27.2	537	15	US-10-425-114-65085 Sequence 65085, A
19	637.5	26.7	508	17	US-10-669-962-17 Sequence 17, Appl
20	634	26.5	509	16	US-10-686-947-260 Sequence 260, App
21	633.5	26.5	503	16	US-10-686-947-198 Sequence 198, App
22	633.5	26.5	503	16	US-10-686-947-262 Sequence 262, App
23	632.5	26.5	504	16	US-10-686-947-196 Sequence 196, App
24	631	26.4	509	16	US-10-686-947-194 Sequence 194, App
25	631	26.4	537	16	US-10-437-963-148695 Sequence 148695,
26	627.5	26.3	495	14	US-10-021-425-29 Sequence 29, Appl
27	627.5	26.3	495	16	US-10-900-856-32 Sequence 32, Appl
28	627	26.2	509	16	US-10-686-947-268 Sequence 268, App
29	626	26.2	512	17	US-10-669-962-6 Sequence 6, Appli
30	625	26.2	502	10	US-09-909-566C-3 Sequence 3, Appli
31	625	26.2	502	16	US-10-759-813-3 Sequence 3, Appli
32	623.5	26.1	516	15	US-10-424-599-145449 Sequence 145449,
33	623	26.1	503	16	US-10-686-947-150 Sequence 150, App
34	623	26.1	513	17	US-10-669-962-15 Sequence 15, Appl
35	622	26.0	516	15	US-10-424-599-145460 Sequence 145460,
36	620.5	26.0	548	16	US-10-437-963-112652 Sequence 112652,
37	619	25.9	503	16	US-10-686-947-152 Sequence 152, App
38	619	25.9	503	16	US-10-686-947-192 Sequence 192, App
39	619	25.9	503	16	US-10-686-947-200 Sequence 200, App
40	618.5	25.9	496	14	US-10-097-559-40 Sequence 40, Appl
41	617.5	25.8	1933	16	US-10-437-963-106209 Sequence 106209,
42	616.5	25.8	500	14	US-10-097-559-39 Sequence 39, Appl
43	616.5	25.8	512	17	US-10-669-962-2 Sequence 2, Appli
44	610	25.5	513	15	US-10-424-599-250650 Sequence 250650,
45	609.5	25.5	506	16	US-10-437-963-112862 Sequence 112862,

ALIGNMENTS

RESULT 1

US-10-310-154-735
; Sequence 735, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Jinzhao
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

Tue May 3 10:43:24 2005

APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 735
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-310-154-735

Query Match 94.4%; Score 2256; DB 15; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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DB 1 MLELALGLLVLALFLHLRPTTAKSKALRHLNPPSPKPRLPFIHGHLLKXLLHYAL 60
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DB 241 DPVVERVVKREIVRRXNGEVEGVSFVLDLTLLEFAEDTKEIKITKHIGLVD 300
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DB 301 FFSAGTSTAVATEWALAEINNPXVLEKAREEYXSVGKDLVDEVDTONLPYIRAIK 360
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DB 361 ETRFMHPPLPVVVKRCXECXINGVIEPEGALILFNWQVGRDPKYWDRPSEKRPFRFLE 420
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DB 421 TGAEGEAGPLDLRGQHFLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPQG 480
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DB 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-10-659-755-2
Sequence 2, Application US/10659755
Publication NO. US20040128711A1
GENERAL INFORMATION:
APPLICANT: Mizutani, Masako
APPLICANT: Kasumi, Takaaki
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Akashi, Tomoyoshi
TITLE OF INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-383
CURRENT APPLICATION NUMBER: US/10/411,115
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/672,785

APPLICANT: DIXON, RICHARD A.
APPLICANT: LIU, CHANG-JUN
APPLICANT: DEAVOURS, BETTINA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
FILE REFERENCE: NBLE:007US
CURRENT APPLICATION NUMBER: US/10/659,755
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,447
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 521
TYPE: PRT
ORGANISM: Soybean
US-10-659-755-2

Query Match 94.2%; Score 2250; DB 16; Length 521;
Best Local Similarity 86.6%; Pred. No. 3.4e-255;
Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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DB 1 MLELALGLLVLALFLHLRPTTAKSKALRHLNPPSPKPRLPFIHGHLLKXLLHYAL 60
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DB 61 IDLSKHGGLFSLXFGSMPTVASTPELFLQTHEATSPXTRFQTSAXRLTYDSSVA 120
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QY 181 KWNSTXSMXKLGEAEIRDIAREVLKIXGEVSLTDPIFLKXKLVGKYEKRIIDILNKF 240
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QY 301 XPSAGXDSTAXTEWALAEINNPXVLXXAREEYXSVGKDLVDEVDTONLPYIRAIK 360
DB 301 FFSAGTSTAVATEWALAEINNPXVLEKAREEYXSVGKDLVDEVDTONLPYIRAIK 360
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RESULT 3
US-10-411-115-4
Sequence 4, Application US/10411115
Publication NO. US2004003431A1
GENERAL INFORMATION:
APPLICANT: Mizutani, Masako
APPLICANT: Kasumi, Takaaki
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Akashi, Tomoyoshi
TITLE OF INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-383
CURRENT APPLICATION NUMBER: US/10/411,115
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/672,785

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; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-10-411-115-4

Query Match      39.5%; Score 944.5; DB 15; Length 512;
Best Local Similarity 38.9%; Pred. No. 1.1e-101;
Matches 193; Conservative 94; Mismatches 182; Indels 27; Gaps 8;

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Db 87 LKTNL-LAFSRKSHSTAIDIVTYSFSAFSPYGYWKFYKIKLCTYELLGARNLGHFQPIR 145
Qy 153 TQQRKRLXMAQXAEAKKPLDXTTEILLKWNSTXSMXL-----GEAEERDIARE 204
Db 146 NLEVRSPFLQLLWHKSFSGESVNVDELVRVLTNSVSHMWSIRCSDEGDAEAARTVIRE 205
Qy 205 VLKIXGYSVLTDFIXPLKXKLVGKYEKRIDDILNKFPDVPVVRVVKRRXIVRRRXNGEXX 264
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Qy 265 EG---EXSGVLDLTLLEFAEDTETXIKTKXXIXGLVVDXFSAGXDSTAXTEWALAEI 321
Db 264 GGGNNEBAKDFDMLLDVMESEGDTEVKTFRHLKALILDFTAGTDTTATATEWALAEI 323
Qy 322 NNXPVLXAXEEXSVVGVKDXLVDVDTQNLPIYRAIVKETFRRMHPPLPVVVKRCXSECK 381
Db 324 NNPNVLKKAQEEISRIIGTKRIVESDAPDLPYLOAIKETFRHLHPPIPLMLSRKSTSDCT 383
Qy 382 INGXXPEGALKXFNVMQVGDXXKYWRDPSEKRPERFLETXAEGAXXLDLRGXHFOLLP 441
Db 384 VNGYKIQAKSLFVNIWISGRNPNYWSPEFRPERFLEKRE----SIDVKGQHFELLP 439
Qy 442 FGSRXMCPCGKXATSGATLASLIQCFDQVLGPOGQILKGDAXKVSMEERAGLTVPR 501
Db 440 FGTRGRCPGMLLAIQEVVSIIGTVMQCDF-----WKLADSGNNVDMTERSGLTAPR 492
Qy 502 AHSILVCVPLARIGVAS 517
Db 493 AFDLVCRLYPRVDPAT 508

RESULT 4
US-10-411-115-2
; Sequence 2, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411.115
```

```
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-10-411-115-2

Query Match      39.4%; Score 940.5; DB 15; Length 506;
Best Local Similarity 39.8%; Pred. No. 3.2e-101;
Matches 196; Conservative 86; Mismatches 185; Indels 25; Gaps 9;

Qy 30 RHLNPPSPXPRLPFIGHXHLKDLHYAXIDLKXKHGPLFSXXFGSMPTVVASTPELFL 89
Db 24 RRKTRPGPL-AUPLIGHLHLGPK-LHHTFHQFSQRYGPIQLYLGSPCVASTPELA 81
Qy 90 KLFQXXEATSEFTRFOTSAKXELTYDXVAXXPXGYPWKFVRKLIWDLKXNATTVNKLRL 149
Db 82 REFLLKTHE-LDFSRKSHSTAIDIVTYSFSAFAPYGYWKFYKIKLCTYELLGARNLGHFQ 140
Qy 150 PLRTOQIRKRLXMAQXAEAKKPLDXTTEILLKWNSTXSMXL-----GEAEERDI 201
Db 141 PIRALEVNSFLRILYEKTEQOSVNVTEELVGLTNSVINMMLGIRCSGTEGEAEVARTV 200
Qy 202 AREVLKIXGYSVLTDFIXPLKXKLVGKYEKRIDDILNKFPDVPVVRVVKRRXIVRRRXNG 261
Db 201 IREVTQIFGDFDSEIVWFCKNDLQIRKSEDIRRYDALLEKIIISDRERL-RLRGGG 259
Qy 262 EXXEGEXSGVXLDLTLLEFAEDTETXIKTKXXIXGLVVDXFSAGXDSTAXTEWALAEI 321
Db 260 GGGGGEVKD-FLDMLLDVMESEKSEVEFTRHLKALILDFTAGTDTTATATEWALAEI 318
Qy 322 NNXPVLXAXEEXSVVGVKDXLVDVDTQNLPIYRAIVKETFRRMHPPLPVVVKRCXSECK 381
Db 319 SNPNVLKKAQEEIMDKVIGSORLQJESDAPNLPYLNAIKETFRHLHPPIPLMLTRKSI 378
Qy 382 INGXXPEGALKXFNVMQVGDXXKYWRDPSEKRPERFLETXAEGAXXLDLRGXHFOLLP 441
Db 379 VNGYTPPAKTLFVNLWSMGRNPNYWNPEFRPERFLEKG----TGSIDVKGQHFELLP 434
Qy 442 FGSRXMCPCGKXATSGATLASLIQCFDQVLGPOGQILKGDAXKVSMEERAGLTVPR 501
Db 435 FGTRGRCPGMLLMQELFSIIGAMVQCFDWKL--PDGV-----KSDVDMTERPGLTAPR 486
Qy 502 AHSILVCVPLARI 513
Db 487 ANDLVCOLVPR 498

RESULT 5
US-10-411-115-8
; Sequence 8, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
```

FILE REFERENCE: 001560-383
CURRENT APPLICATION NUMBER: US/10/411,115
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/672,785
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JPO0/04379
PRIOR FILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/JPO0/00490
PRIOR FILING DATE: 1999-01-28
PRIOR APPLICATION NUMBER: JP 11-205229
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: JP 11-22427
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.0
SEQ ID NO 8
LENGTH: 506
TYPE: PRT
ORGANISM: Perilla frutescens
FEATURE:
OTHER INFORMATION: Amino acid sequence of a protein having an activity to
US-10-411-115-8
OTHER INFORMATION: directly convert flavanone to flavone

Query Match 38.6%; Score 921.5; DB 15; Length 506;
Best Local Similarity 38.9%; Pred. No. 5.6e-99;
Matches 190; Conservative 91; Mismatches 183; Indels 25; Gaps 8;
QY 33 PNPSPRLPFIQHXHLLKDKLLHYAXIDLSKXGKPLFSXXFGSMPTVASTPELPLKF 92
DB 27 PYPGPFP-LPIIHLHLGPR-LHQTPHDLQRYGPLQMLRLGSIKRVIAAASPELAKEC 84
QY 93 LQXEAESFTRFOTSAKRLTYDXVAXXPXGPMVFXVRLINMDLXNATTVNXLPLR 152
DB 85 LKTHLV-FSRKSTAIIVTSDSFAPSYGPMVFXVRLINMDLXNATTVNXLPLR 143
QY 153 TQIKRLXMAOXAAXKPLDXTTELLKXNNTXSMWXL-----GEAEIRDARE 204
DB 144 TLEVKSLQILMRKSGESGFNTEELVKLTSNVISHMWSLIRCSSETSSEAEARTVIRE 203
QY 205 VLKIXGEYSLTDFXPLKXKLVGYKXKIDILNKFPVVERVTKKRXIVRRXNGEXX 264
DB 204 VTQIFGEFVDSIIWLCKNFQGIKRSEDIQRRYDALLEKIITDREK--QRRTHGGG 261
QY 265 EGXSGVKLDTLLEFADETXEIKITKXIXGLVVDXFSAGXSDTAXXTWALAEINNP 324
DB 262 GGGAEPDLNFDLIMESGKAEVFTREHLKALILDFEFTAGTDTTAVCEWATAEVINNP 321
QY 325 XVLXAREEYXSVVGKDXLDEVDTONLPYIRAIKVTETFRMHPPPLPVVKKKXEECXING 384
DB 322 NVLKAQAEIANIVGDFRILQESDAPNLPLYQALIKETFRHLPPIMLARKSISDCVIDG 381
QY 385 XVXPEGALXPNVWQVXGXKWDYRPSXPERPLETYAAGEAXXLDLKGXHFQLLPFGS 444
DB 382 YMIPIANTLLFVNLWSMGRNPKINDYPTAFQPERLEK---EKAAIDVKGQHPFLLPFGT 437
QY 445 GRXKCPGVXLSATSCXATLLASLIQCFDLOVLGQKILKXDAKVSMEERAGLTVPEAHS 504
DB 438 GRRCCPGLMLAQEVVIGMIQCFDWKL--PDG-----SGHVDMAERPGLTAPRET 489
QY 505 LVCVPLARI 513
DB 490 LFCRVVPRV 498

RESULT 6

US-10-424-599-149724
Sequence 149724, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149724
LENGTH: 509
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_106222C.1.pap
US-10-424-599-149724

Query Match 38.5%; Score 919.5; DB 15; Length 509;
Best Local Similarity 39.8%; Pred. No. 9.6e-99;
Matches 198; Conservative 86; Mismatches 184; Indels 29; Gaps 9;
QY 29 LRHLPPPPSPXPR-LPFIQHXHLLKDKLLHYAXIDLSKXGKPLFSXXFGSMPTVASTPE 87
DB 30 LRHKPRRP-FGPKSLPFIIGHHLI-SALPHQSFHALSTRYGPVAVQVFLGSPVAVVWSCE 87
QY 88 LFKLFLQXBEATSFXTRFOTSAKRLTY-DXVAXXPXGPMVFXVRLINMDLXNATTVN 146
DB 88 LAKEFLKTHE-PSFSNRFSAAVHHLSYSGKGFAPYGSYWFPLKICMSSELLGGRTLD 146
QY 147 XLRLPTQIIRKRLXMAOXAAXKPLDXTTELLKXNNTXSMWXL-----GEAEI 198
DB 147 QFRHLREQETLRLFLVLRKAGEAHEAVDSGELMTLTNSVISRMVLSTRTCCESDGDVEHV 206
QY 199 RDIAREVLKIXGEYSLTDFXPLKXKLVGYKXKIDILNKFPVVERVTKKRXIVRRR 258
DB 207 RRVADTAELAGKFNLAADFVWLCKGLDLHGKIKRLVGLERFDGMDRVRIREHEERERR 266
QY 259 XNGEXEGEXSGVKLDTLLEFADETXEIKITKXIXGLVVDXFSAGXSDTAXXTWALA 318
DB 267 K--ERGEGERDILLDILHDESEIKLSRENVKAFILDIYMACTDTSATMEWALA 324
QY 319 ELINNPXVLXAREEYXSVVGKDXLDEVDTONLPYIRAIKVTETFRMHPPPLPVVKKKX 378
DB 325 ELINNHVMEKARQEDISVTGNKRLIQESDLPNLPYLOAIVKETLRIHTPTAPLLGRESSE 384
QY 379 ECKINGXVXPEGALXPNVWQVXGXKWDYRPSXPERPLETYAAGEAXXLDLKGXHFQ 438
DB 385 SCNVCGDIPAKSLVFNWLSMGRDPEKIMWEDPLEFPERFMN---NNEDKQIDVRGQNFQ 441
QY 439 LLPFGSGRXKCPGVXLSATSCXATLLASLIQCFDLOVLGQKILKXDAKVSMEERAGL 498
DB 442 LLPFGTGRRLCPGASLALQTVPTNVAAMLQCFEFRV-----DGTVSMEERKPMAT 490
QY 499 VPAHSLVCVPLARI 515
DB 491 LPRAPHLICVVPVRMNL 507

RESULT 7

US-10-424-599-221409
Sequence 221409, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 221409
LENGTH: 509

```
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(509)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41962C.1.pap
US-10-424-599-221409

Query Match      37.3%; Score 891.5; DB 15; Length 509;
Best Local Similarity 38.4%; Pred. No. 1.9e-95;
Matches 188; Conservative 92; Mismatches 183; Indels 27; Gaps 8;

Qy 35 PPSXPRLPFIIGHXHLKDLXLLHYAXIDLKXKHGFLFSXXFGSMPTVASTPELFLQ 94
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 PPSMP-LPIIIGHLHLV-SPIPHQDFYKLSRHHGPIIMQLFLGSPVPCVASTAAEAKFLK 87
Qy 95 XEATSFTRFQTSAXRXLTYDX---VXVAXPXGPYKXFKVRLIMNDLXNATTVNXLRLP 151
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
88 THEINFNSRPGQNVAVKGLAYDSQDFLFAFPFGPYKFKMKKLCWSELSSGRMMDQLPV 147
Qy 152 RTQIRKXLRMAQXAEAKPLDXTEELLKWNSTXMMXL-----GEABEIRDIAR 203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
148 RXQETKRFISVRKGVAGEAVDFGDELTMTLSNNIVSRMTLSQKTSENDNQAEEMKKLVS 207
Qy 204 EVLKIXGEYSITDFIXPLKXKLVKGYEKRIDDIILNKFPVVERVIKRRXIVRRRXNGEX 263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
208 NIAELMGKFNVSDFIWLKPDLOGFNKIKETRDREDVVDGIIKQRE--ERRKNKET 265
Qy 264 XEEXSGVKVLTLLLEFADETXEIKITKXXIXGLVVDXFSAGXSDTAXXTWALAEINN 323
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
266 GTARQKMDLVLDIGDSDSEIKLTKENIKAFIMDFIVAGTDTSAATMEWMAELINN 325
Qy 324 PXVLXXAREEYXSVGKDXLVDVDTQNLPIYIRAIKVTFRMHPLPVKREKXEECXIN 383
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
326 PYVLEKARQEDAVVGSRMVEESDIANLPIYQIAVRETLLRHPGGVLVRESSKSAVVC 385
Qy 384 GXVPEGALXXFNVMQVGDXXKWDPRSEKPERPLETXAEAGXIXDLRGXHFQLLPFG 443
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
386 GYDIPAKTRLFVNVWAIGRDPNHWEKPEFPERFIR---DQO-NQLDVRGQHYHFIPFG 441
Qy 444 SGRXWCPGVXLATSGXATLLASLQCFDVLQVGPQILKXGDAKXVMEERAGLTVPRAH 503
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
442 SGRRTCPGASLAWQVVPVNLAIQCFOWKLVGGNG-----KVDMEKSGITLPRAN 493
Qy 504 SLVVCVPLARI 513
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-10-424-599-263430
; Sequence 263430, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263430
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7989C.1.pap
US-10-424-599-263430
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(509)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41962C.1.pap
US-10-424-599-221409

Query Match      36.4%; Score 870; DB 15; Length 510;
Best Local Similarity 38.7%; Pred. No. 6.4e-93;
Matches 189; Conservative 82; Mismatches 192; Indels 26; Gaps 8;

Qy 35 PPSXPRLPFIIGHXHLKDLXLLHYAXIDLKXKHGFLFSXXFGSMPTVASTPELFLQ 94
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
32 PPSMP-LPIIIGHLHLV-SPIPHQDFYKLSRHHGPIIMQLFLGSPVPCVASTAAEAKFLK 89
Qy 95 XEATSFTRFQTSAXRXLTY-DXXVAXXPXGPYKXFKVRLIMNDLXNATTVNXLRLPRT 153
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 THEPAPSNRRPANTVAVETLTYASEDFLFAFPFGPYKFKMKKLCWSELSSGRMMDQLPV 149
Qy 154 QOIRKXLRMAQXAEAKPLDXTEELLKWNSTXMMXL-----GEABEIRDIARE 204
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 QETKFKFIRKVLQKIGSEAVDFGGEFTTLSNNIVSRMIVSQTSTEDENEVEEMKLVKD 209
Qy 205 VLKIXGEYSITDFIXPLKXKLVKGYEKRIDDIILNKFPVVERVIKRRXIVRRRXNGEX 264
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
210 AELSGKFNISDFVSLKRFDLQGFNKRLEKIRDCFDVILDRIRIKQRE--ERRKNKET 268
Qy 265 EGEKSGVKVLTLLLEFADETXEIKITKXXIXGLVVDXFSAGXSDTAXXTWALAEINN 324
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
269 KRLEKDM-LDVLFDISESESEIKENKANIILDLIAGTDSAVTMEWMAELINN 327
Qy 325 XVLXXAREEYXSVGKDXLVDVDTQNLPIYIRAIKVTFRMHPLPVKREKXEECXIN 384
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 GVLEKARQEDAVVGSRMVEESDIANLPIYQIAVRETLLRHPAGPLLFRESSRAVVC 387
Qy 385 XVPPEGALXXFNVMQVGDXXKWDPRSEKPERPLETXAEAGXIXDLRGXHFQLLPFG 444
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
388 YDIPAKTRLFVNVWAIGRDPNHWEKPEFPERFVENG----KSQLDVRGQHYHLLPFG 443
Qy 445 GRXWCPGVXLATSGXATLLASLQCFDVLQVGPQILKXGDAKXVMEERAGLTVPRAHS 504
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
444 GRACPTSLALQVHVHNLAVLQCFOWKLVDCDNG-----KVNMEKAGITLPRAP 495
Qy 505 LVCVPLARI 513
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
496 IICVPPIRL 504

RESULT 9
US-10-424-599-244810
; Sequence 244810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 244810
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63093C.1.pap
US-10-424-599-244810

Query Match      35.3%; Score 843; DB 15; Length 502;
Best Local Similarity 38.0%; Pred. No. 9.4e-90;
Matches 185; Conservative 84; Mismatches 190; Indels 28; Gaps 8;

Qy 35 PPSXPRLPFIIGHXHLKDLXLLHYAXIDLKXKHGFLFSXXFGSMPTVASTPELFLQ 94
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 PPSMP-KGLPIIGHLHLV-SPIPHQDFYKLSRHHGPIIMQLFLGSPVPCVASTAAEAKFLK 87
```


Db 188 NSIMRWASALPGEMAEARCAKQVAELVGAFAEDFVAVCRGWDLOGIGRRNEVHAR 247
Qy 240 FDPVVERVVKRRXITVRRRXNGEXXGKXGVKLDLTLEFADETXEIKTKXXIXGLV 299
Db 248 FDALLETIEAKEE-ARRSLRGRRSSKDLMLDAAEDDTAEVKLTEDNIKAFVL 306
Qy 300 DXFSAGXSTAXXTWALAEILNPNKVLXAXREXYSGVKDXLVEVDTONLPYIRAV 359
Db 307 DIFTAGSDTTATTVEWMLAEILVNHPECMAKRLGELDAVVGSRSLVGEQDVARLPYLA 366
Qy 360 KETFMHPPLPVKHKKEEXKXGKXVPEGALXKXFNWQVXDXKXWDRSEKXRPFL 419
Db 367 KETLRPAPVPAQVTVPEVQVRGTYTPTDQVFFNISGRDATTYWDQDHPDRFL 426
Qy 420 ETXAEAXXLDLRGHFQLPFGSGRXMCVGLATSGXATLLASLQCFDLQVLGPOG 479
Db 427 ---PDGAGATVDPKQHPQLMPFGSGRRACPGMLAMQAVPAFLAALVQCFDW--APPS 481
Qy 480 QILKXDAKXMEERAGLTVFRAHSLVCUPLARI 513
Db 482 QPL-----PLDMEEAAGLVASARKHPLLLPTPRI 510

RESULT 12

US-10-437-963-169616
; Sequence 169616, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169616
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68019C.1.pap
US-10-437-963-169616

Query Match 30.6%; Score 730.5; DB 16; Length 516;
Best Local Similarity 35.3%; Pred. No. 1.7e-76;
Matches 169; Conservative 79; Mismatches 204; Indels 27; Gaps 11;
Qy 35 PPSPXPRLPFTGHXHLKDLHYAXIDLSKXGKPLFSXFGSMPTVVAATPELFLQ 94
Db 44 PPSPA-SLPVIGHLHLRPP-VHRTFHAEARLGLPMLVRLGSHCVVASSAEVAELIR 101
Qy 95 XEATSFYTRFQTSAXRLTYDXX-VAXXPXGPYKXFKRLIMNDLXNATVNXLRPLRT 153
Db 102 SHEA-KISERPLTAVARQFAYESAGFAPYSPHWRFMKRLCMSSELLGRTVEQLRPVR 160
Qy 154 QOIRKXLRMAQXAEAXKPLDXTBELLKXNXTXSMXILGE-----AEEIRDIAREVLKI 208
Db 161 AGLVSLRLHVLISQPEA-EAVDUTRELIRMSNTSITIRMAASTVPSSVTEAEQELVKVVAEL 219
Qy 209 XGEYSLDFIXPLKXKLVKYEKRIIDDILNKFPDPPVERVVKRRXIVRRRXNGEXXGEX 268
Db 220 VGFANADDYIALCRGWDIQLGERRAADVHKRFDALLEEMIRKHEE-ARMKKTDTDVG-- 276
Qy 269 SGVXLDTLLEFADETXEIKTKXXIXGLVVDXFSAGXSTAXXTWALAEILNPNKVLX 328
Db 277 SKDLIDLDAEDGAAEVKLTEDNIKAFIIDDVVTAGSDTSAAMVEMVMAELMNHPEALR 336

Qy 329 XAREEXYSVVGKDXLVEVDTONLPYIRAVKETFRMHPPLPVVVKRCKEBCXINGXYXP 388
Db 337 KVREEIEAVVGRDRRIAGEGDLPLPYLQAAYKETLRLRPAAPIAHQSTEEIQRGFRVP 396
Qy 389 EGALXXFNWQVQVXDXKXWDRSEKXRPFLFETXAEAXXLDLRGHFOLLPGSGRXM 448
Db 397 AQTAFFINVAIGRDPAYWEEPLFRPERFL---AGGGEGVEPRGQHFQMPFGSGRRG 453
Qy 449 CPGVKLTATSGXATLLASLQCFDLQVLGPOQIILKXDAK-VSMEEERAGLTVFRAHSLV 506
Db 454 CPGMLALQSPVAVVAALLQCFDWQCM-----DNKLIDMEADGLVCARKHLL 502

RESULT 13

US-10-424-599-243352
; Sequence 243352, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243352
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61775C.1.pap
US-10-424-599-243352

Query Match 30.0%; Score 717; DB 15; Length 513;
Best Local Similarity 34.3%; Pred. No. 6.3e-75;
Matches 170; Conservative 78; Mismatches 224; Indels 24; Gaps 8;
Qy 27 KALRHLPNPPSPXPRLPFGHGHLLKDLHYAXIDLSKXGKPLFSXFGSMPTVASTP 86
Db 26 KKPQRLRPLPGPPIISIPLLGHAPYLR-SLLHQALYKLSLRYGPLIHVMIGSKHVVA 84
Qy 87 ELFKLELQXXEATSFYTRFQTSAXRLTYDXX-VAXXPXGPYKXFKRLIMNDLXNATV 145
Db 85 ETAKQILKTSE-EAFNCRPLMIASESLTYGAADYFFIPYGYWRFLKLCMTTELLSGK 143
Qy 146 NXLRPLRTOQIRKXLRMAQ-XAEAXKPLDXTBELLKXNXTXSMXILG-----BAE 196
Db 144 EHFVRIRESEVEAFKRMWEISGNGYEVVWRKELITHTNITRMINGKKSNAENDEVA 203
Qy 197 EIRDIAREVLKIXEYSLTFIXPLKXKLVKYEKRIIDDILNKFPDPPVERVVKRRXIVR 256
Db 204 RLKRVVREVGELLGAFNLGDIVGFMRLDLOGFGKQNMETHHKKVDAMMEKVLREHEA 263
Qy 257 RXNGEXXGEXSGVXLDTLLEFADETXEIKTKXXIXGLVVDXFSAGXSTAXXTWA 316
Db 264 K-----EADSRKDKDLFDILNLTADGADNKLITRESAKAFALDMFINGTPASVL 319
Qy 317 LAELINPNVLXAXREEXYSVVGKDXLVEVDTONLPYIRAVKETFRMHPPLPVVVKRKC 376
Db 320 LAELVRNPHVFKAREEIESVVGKRLVKESDIPNLVYLQAVLKETLRLHPTPIFAREA 379
Qy 377 XEECXINGXVPEGALXKXFNWQVXDXKXWDRSEKXRPFLFETXAEAXXLDLRGXH 436
Db 380 MRTQVEGYDIPENSTILISTWAGRDPNWDALVYKPERFLFSDDPGKS-KIDVRGOY 438
Qy 437 FOLLPGSGRXMCVGLATSGXATLLASLQCFDLQVLGPOQIILKXDAKXMEERAG 496
Db 439 YOLLPGSGRRSCPGASLALLVMQATLASLQCFDWIV-----NDGNHHHVDMSBGR 491

Qy 497 LTVPRASHLVCVPLAR 512
Db 492 VTVFLAKLCKPVP 507

RESULT 14

US-10-424-599-258259
; Sequence 258259, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258259
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75231C.1.pap

US-10-424-599-258259

Query Match 29.4%; Score 701.5; DB 15; Length 509;
Best Local Similarity 32.6%; Pred. No. 4.2e-72;
Matches 169; Conservative 82; Mismatches 227; Indels 41; Gaps 12;

Qy 11 VLALFXHLRPPXAXSKALRHLNPPSPXPLPFIGHXHLKDKLLHYAXIDLSKKHGL 70
Db 5 IVFLFLLLSLISSSSNNLSQLPPSP-PSIPLLGHHLTPS-LYKSLYTLSSKRGPL 62
Qy 71 FSXXFGS-----MPTVVASPELFFK---LFLQXKEATSPFTR--FOTSAXRXLTYDXV 119
Db 63 LLLRLGFSRRLLLVSSNAATDVFKTHDLAFSPAPAFARLPFGTSG-----F 113
Qy 120 AXXPXGYPWPFVKLIMNDLNATTVNKLRLPRTQQIRKXLRMAQXAEAKPLDXTEEL 179
Db 114 VTAPYGPYRPMKKLCVTELLSTQLRSRSIRREELRSIKRVIDNARETVALLDLSGF 173
Qy 180 LKWN-----STXSMXIGEAEIRDIAREVLKIXGEVSLTDFTXPLKXKLVGKYEK 231
Db 174 TKFTNNVTCTAMSTSCAEKCEDAERIRKLVKESFELAAKLCFGDVLGPFKLSFWYVGK 233
Qy 232 RIDDLNKFDPVVERVIRRRXNGEXXEGXSGVKLDTLLEFAEDT-XEIKITK 291
Db 234 KAIDMSTRYDELLBEVLKEHEKELSRANGDSESD---LMDILLDVYHDAHAEFKITM 289
Qy 292 XXIXGLVVDPSAGSDTAXTEWALAEELNNPVLXXAREEYXSVVGKDXLDEVDTON 351
Db 290 AHIAKAFMDLFIAGTHTSABATOWAMAEELNHPAFQKVRKEITELVTGNVRLVDESITN 349
Qy 352 LPYIRATVKTETFRMHPPLPVVKKCECKXNGXVXEPGALXXPNVQVGDXXKXWDPS 411
Db 350 LPYLQAVVKETLRYLPAPITTTRECRHCKINSFDPVPPKTAVALNIAIMRDPDSWDNPN 409
Qy 412 EXPRERLETXAEGEAXKLDLRGHFQLLPFGSGRXCPCGVXLATSGXATILLASLIQCFD 471
Db 410 EFCFERLQ-EQDHEDLSDDGKMKFNFPVFGGGRCCPGTALAFSLMNTAVAAWVQCFD 468
Qy 472 LQVLGPGQILKXKDAKVSMEERAGLTVPRASHLVCVPL 510
Db 469 WKI-GKDG---KG--EKVDMESGSGMSLVMHPLICVPV 501

RESULT 15

US-10-425-114-64368
; Sequence 64368, Application US/10425114
; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64368
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-223-H4_FLI.pap
US-10-425-114-64368

Query Match 28.9%; Score 691.5; DB 15; Length 548;
Best Local Similarity 34.9%; Pred. No. 6.9e-72;
Matches 177; Conservative 77; Mismatches 208; Indels 45; Gaps 14;

Qy 26 SKALRHLNPPSPXPLPFIGHXHLKDKLLHYAXIDLSKKHGLPSXXFGSMPTVAST 85
Db 55 ARSTRKYRLPPGPRP-WPVIGNLNLI-GPLPHSHVHLSKRYGLPLMSLRFSGFPVVVASS 112
Qy 86 PELFKLPLOXKEATSPFTRPOTSAXRXLTYD-XKVAAXXPXGPYWXFVRKLIIMDLNAT 144
Db 113 VDTARLLIKTHD-LAFIDRPQTAAGRYTYNCAGLFPQYGVAYWQARRLCOAELFSARR 171
Qy 145 VNKLRLPRTQQIRKXLRMAQXAE-----XKPLDXTTEELKWNXNYSXMMXIGE----- 194
Db 172 LMSLEHVRSEDEVRAMLSRLRAASSAPAGGHDAVTLREHLYMWNLSVVSRLMLGKYYVEG 231
Qy 195 -----AEIRDITAREVLKIXGEVSLTDFTXPLKXKLVGKYEKRIIDILNKFPVVERVI 248
Db 232 SSSPAPTEEPFRWLIDHEFFLNGVLNVADMPLWLSPLDPQGYVRMRKRSACKMLDRFLEHV 291
Qy 249 KKRXXIVRRXNGEXXEGXSGVKLDTLLEFAEDT-XEIKITKXIXGLVVDXFSAGXD 307
Db 292 DEHNE-RRRREGEDFVAMD---MMDVLELADDPQLEVPITRDNVKGFPTLDMGGGTD 346
Qy 308 STAXXTWALAEELNNPVLXXAREEYXSVVGKDXLDEVDTONLPYIRATVKTETFRMHP 367
Db 347 TSAVTVEWAMSELLRNPEVLAKATEELDRVVGDRDLVAEGDIPSLPYLDAVVKETLRLHP 406
Qy 368 PLPVV-KRKCEKXNGXVXEPGALXXFNWQVGDXXKYWDRPSRXRPERLETXAEGE 426
Db 407 VAPLLTFLRCREDVSGGYDIPAGARVFNVAIGRDPVAVEAPLEFRPRF-----A 459
Qy 427 AXKLDLRGHFQLLPFGSGRXCPCGVXLATSGXATILLASLIQCFDQLVLGPGQILKXGD 486
Db 460 GSSVDVKGQHFELLFPFGSGRXCPCGMGLALRMVPTILGNLLHAFANRL--PDGVAAB--- 514
Qy 487 AKVSMEERAGLTVPRASHLVCVPLARI 513
Db 515 -ELGMEETGLTVPR-----LVPLQAV 535

Search completed: April 29, 2005, 17:34:24
Job time : 83 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2005, 17:31:50 ; Search time 268 Seconds
(without alignments)
3180.971 Million cell updates/sec

Title: US-09-857-581B-66
Perfect score: 2389
Sequence: 1 MLELALGLXVLAFLXHLRP.....AHSLVCPVLARIGVASKLS 521

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/h/US09857581/runat.29042005.104822.20983/app_query.fasta.1.711
-DB=Issued_Patents_NA -QWMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCTL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857581.qcgn.1.1.69 @runat.29042005.104822.20983 -NCPU=6 -ICPU=3
-NO.MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	94.2	1824	3	US-08-948-564-13
2	944.5	39.5	1730	4	US-09-672-785-3
3	943.5	39.5	1724	4	US-09-672-785-1
4	921.5	38.6	1770	4	US-09-672-785-7
5	637.5	26.7	1660	4	US-09-142-108C-16
6	629	26.3	1488	4	US-09-689-783A-1
7	626	26.2	1711	4	US-09-142-108C-5
8	625	26.2	1781	3	US-09-499-302A-1
9	623	26.1	1748	4	US-09-142-108C-14
10	618.5	25.9	1762	3	US-08-881-784-5
11	618.5	25.9	1762	3	US-09-292-768-1
12	618.5	25.9	1762	3	US-09-292-768-65

13	618	25.9	1806	3	US-09-351-229-3
14	616.5	25.8	1665	3	US-08-881-784-8
15	616.5	25.8	1665	3	US-09-292-768-3
16	616.5	25.8	1665	3	US-09-292-768-67
17	616.5	25.8	1789	4	US-09-142-108C-1
18	615.5	25.8	1665	3	US-09-292-768-69
19	613.5	25.7	1762	3	US-09-292-768-63
20	606.5	25.4	1762	3	US-09-172-339-5
21	600.5	25.1	1515	3	US-09-292-768-5
22	593	24.8	1815	4	US-09-142-108C-18
23	590.5	24.7	1737	4	US-09-142-108C-3
24	590	24.7	1824	4	US-09-142-108C-20
25	583	24.4	1657	3	US-08-948-564-11
26	578.5	24.2	1722	3	US-09-033-055A-1
27	574	24.0	1757	1	US-08-313-075A-49
28	574	24.0	1757	4	US-09-142-108C-26
29	571.5	23.9	2174	3	US-08-606-505B-63
30	571.5	23.9	2174	3	US-09-616-990-63
31	567	23.7	1667	4	US-09-142-108C-22
32	566.5	23.7	1665	1	US-08-313-075A-29
33	565.5	23.7	1893	1	US-08-532-065B-1
34	564.5	23.6	1927	3	US-08-606-505B-64
35	564.5	23.6	1927	3	US-09-616-990-64
36	563.5	23.6	1812	1	US-08-313-075A-37
37	563.5	23.6	1824	3	US-08-606-505B-1
38	563.5	23.6	1824	3	US-09-616-990-1
39	559.5	23.4	2013	3	US-09-615-192A-404
40	557.5	23.3	1634	3	US-09-126-420A-2
41	556.5	23.3	1737	3	US-09-136-420A-1
42	556.5	23.3	1838	2	US-09-081-432-1
43	556.5	23.3	1838	4	US-09-387-663-1
44	556.5	23.3	1838	4	US-09-214-139B-2
45	555.5	23.3	1691	3	US-08-948-564-3

ALIGNMENTS

RESULT 1

US-08-948-564-13
; Sequence 13, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1824 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 54..1616
 ; US-08-948-564-13

Alignment Scores:

Pred. No.: 1.75e-301 Length: 1824
 Score: 2250.00 Matches: 451
 Percent Similarity: 86.56% Conservative: 0
 Best Local Similarity: 86.56% Mismatches: 70
 Query Match: 94.18% Indels: 0
 DB: 3 Gaps: 0

US-09-857-581B-66 (1-521) x US-08-948-564-13 (1-1824)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
 Db 54 ATGTTGCTTGAACCTTGCATTTGGTTTATTTGGCTCTGTTTCTGCACTTTCGCTCCC 113
 Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
 Db 114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCAAACCCCAACGCCCAAGCCT 173
 Qy 41 ArgLeuProPheLeuGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 174 CGTCTCCCTTCATAGACACCTTCACTCTCTTAAAGACAAACTTCTCCACTAGCACTC 233
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 234 ATCCACCTCTCCAAAAAACAATGGTCCCTTATCTCTCTACTTCTGCTCCATGCCAAC 293
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 294 GTTGTTCCTTCCACACAGAAATGTTCAAGCTCTTCTCCAAACGACGAGGCACTTCC 353
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 354 TTCAACCAAGTTTCCAAACCTCAGCCATAAGACGCTCCTACCTATGATAGCTCAGTGCC 413
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140
 Db 414 ATGGTTCCCTTCGGACCTTACTGGAAGTTCTGAGGAAGCTCATCATGAACGACCTTCCC 473
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 474 AACGCCACCACTGTAAACAAGTTGAGGCCCTTTGAGGACCCCAACGACCCCGAAGTTCCTT 533
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 534 AGGTTATGCCCCAAGCGCAGAGGCCACAGAGCCCTTGCATTGACCGAGGAGCTTCTG 593
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 Db 594 AAATGGACCAACACACCATCTCCATGATGCTCGCGAGGCTGAGGAGATCAGAGAC 653
 Qy 201 IleAlaArgGluValLeuLysIle***GlyLysTrpSerLeuThrAspPheIle***Pro 220
 Db 654 ATCGCTCGCAGGTTCTTAAGACTTTTGGCAATACAGCTCTCACTGATCTTCACTGCGCCA 713
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspPheLeuAsnLysPhe 240
 Db 714 TTGAAGCATCTCAAGGTTGGAAGATATGAGAAGGATCAGACGACATCTTGAACAAGTTC 773
 Qy 241 AspProValGluArgValIleLysLysArg***IleValArgArgArg***Asn 260
 Db 774 GACCTCTCGTTGAAGGGGTCATCAAGAAGCGCGTGAGATCGTGAGGAGAGAAAGAC 833
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280

Db 834 GGAGAGTTGTTGAGGGTGAAGTCAGCGGGTCTTCTTGACACCTTCTTGATTGCT 893
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
 Db 894 GAGGATGAGACCATGGAGATCAAAATCACCAGGACCACATCGAGGGTCTTGTGTGCGAC 953
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 Db 954 TTTTCTCTCGCAGAGAACAGACTCCACAGCGGTGGCAACAGAGTGGCGATTTGGCAGAACTC 1013
 Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 Db 1014 ATCAACATCTTAAGGTGTTGAAAAGGCTCTGAGAGAGTCTACAGTGTGTGGGAAAG 1073
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 Db 1074 GACAGACTTGTGACGAAGTTGACACTCAAAACCTTCTTACATTAGAGCAATCGTGAAG 1133
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 Db 1134 GAGACATTCGCGATGCAACCGCCACTCCCAAGTGGTCAAAAGAAAGTGCACAGAGAGTGT 1193
 Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTyrGlnVal 400
 Db 1194 GAGATTAAATGATATGTGATCCCAAGGAGGAGCAATTGATCTCTTCAATGTATGGCAAGTA 1253
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 Db 1254 GGAAGAGACCCCAATACTGGGACAGACCATCGAGTTCGCTCTGAGAGGTTCTTAGAG 1313
 Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 Db 1314 ACAGGGCTGGAAGGGAAGCAGCGCTTGTGATCTTAGGGGCAACATTTTCAACTTCTC 1373
 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 Db 1374 CCATTTGGGTCTGGGAGGAGATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1433
 Qy 461 ThrLeuLeuAlaSerLeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 Db 1434 ACATTTCTTGCATCTCTTATTCAGTCTGCTGACTTGCAGTGTGGGTCCCAAGGACAG 1493
 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 Db 1494 ATATTGAAGGGTGGTCAAGCAAGTAGCATGGAAGAGAGAGCCGCGCTCACTGTTC 1553
 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
 Db 1554 AGGCAATAGTCTTCTGTGTTCCTTGCAGGATCGGCGTTGCACTAACTCCTT 1613
 Qy 521 Ser 521
 Db 1614 TCT 1616

RESULT 2

US-09-672-785-3
 ; Sequence 3, Application US/09672785
 ; Patent No. 6596927
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako
 ; APPLICANT: Kasumi, Takaaki
 ; APPLICANT: Ayabe, Shin-ichi
 ; APPLICANT: Akashi, Tomoyoshi
 ; TITLE OF INVENTION: Genes Coding for Flavone Synthases
 ; FILE REFERENCE: 001560-383
 ; CURRENT APPLICATION NUMBER: US/09/672, 785
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
 ; PRIOR FILING DATE: 2000-01-30
 ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: JP 11-205229

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; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0.
; SEQ ID NO 3
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-09-672-785-3

Alignment Scores:
Pred. No.: 2,2e-120 Length: 1730
Score: 944.50 Matches: 198
Percent Similarity: 57.56% Conservative: 95
Best Local Similarity: 38.90% Mismatches: 189
Query Match: 39.54% Indels: 28
DB: 4 Gaps: 8

US-09-857-581B-66 (1-521) x US-09-672-785-3 (1-1730)

Qy 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro*** 39
Db 103 CCACCACCTTCTCTCTCTCTCTCGCGCGA-AGGGAGCACCGTCTCGCGCGGCTCTCTC 161
Qy 40 ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla 59
Db 162 ---TCCCTTACCATAATTTGGCCACCTCCACCTCTCTCGGCCCAAGA---CTCCACACACG 215
Qy 60 ***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetPro 79
Db 216 TTCATGAATTTCTACTCAATATACGGCCCATATGATCCAGCTCAAGCTCGGCTCGATCCG 275
Qy 80 ThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThr 99
Db 276 TGGTGTGGTCTCGACGCCCGAGCTCGGAGAGATTCTTAAGACGAACGAG---CTC 332
Qy 100 SerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****Val 119
Db 333 CGGTCTCTCTCGCAAGCACTCTACGCGCCATAGACATCGTCACGACTCGTCTCTTT 392
Qy 120 Ala*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu 139
Db 393 GCTTTCTCTCGTACGGACCTTACTGGAAGTACATCAGAAACTGTGTACTACGAGCTG 452
Qy 140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
Db 453 CTCGGAGCGGAACCTCGGACACTTTTCAGCCCATAGGAATCTCGAGGTCTCGTCTTT 512
Qy 160 LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
Db 513 CTGCAGCTTCTGATGTCACAGAGCTTTAAAGGGCGAGAGTGTGAATGTGCACAGACGAGCTG 572
Qy 180 LeuLysTrp***AsnSerThr***SerMetMet***Leu----- 192
Db 573 GTGAGGTGACGAGCAATGTGATATCCACATGATGCTGACATAGGTCTCGGAAGAT 632
Qy 193 ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGlu 211
Db 633 GAAGCGATGCTGAGCGCGCGAGACAGTGTATCGCGAGGTGACGAGATATTGGGGA 692
Qy 212 TyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGlyLys 231
Db 693 TTCCATGTTACGAGCAATAATATGTTTGCAGAAATTCGATCTCTCGCGGGATAAAGAAG 752
Qy 232 ArgIleAspAspIleLeuAsnLysPheAspProValGluArgValIleLysLysArg 251
Db 753 AGGTACAGAGATATTCAGAGAGGATGATGCTTTGCTCGAAGATATTAGTAGTAGA 812
Qy 252 Arg***IleValArgArg***AsnGlyGlu*****GluGly-----Glu*** 268

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Db 813 GAGAGA-----TCGAGGAGGCAAAATCGTATAAGCATGTGCGGTAACAATGAGGAG 866
Qy 269 SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLys 288
Db 867 GCCAAGGATTTCTTGATATGTTGCTTGTATGATGGAGAGTGGGACACCGAGGTCAAA 926
Qy 289 IleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSer 308
Db 927 TTCACTAGAGAGCATCTCAAGGCTTTGATCTGTGATTTCTTCAGCGCGGTACGACACA 986
Qy 309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
Db 987 ACAGCCATAGCACCGAGTGGGCCATCGCGAGCTCATCAACAACCCGAACTCTTGAAG 1046
Qy 329 ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
Db 1047 AAGCCCCAAGAAGAAATATCCCGGATCATCCGAACCAAGCGGATCGTACAAGAATCCGAC 1106
Qy 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
Db 1107 GCCCCAGACCTACCTTACCTCCAGGCCATCATCAAGGAGAGCTTCCGGCTCCACCACCG 1166
Qy 369 LeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
Db 1167 ATCCCGATGCTCTCGCTAGTCCACCTCCGATTGCACGGTCAACGGCTACAAAATCCAA 1226
Qy 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
Db 1227 GCCAAGAGCTCTTGTTCGTGAACATATGTTCCATCGTTCGAAACCCCTTAATTACTGGAA 1286
Qy 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
Db 1287 AGCCTATGAGTTCAGCGCCGAGCGGTTCTTGAGAGGAGCGCGAG----- 1334
Qy 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
Db 1335 TCATCGACGCTCAAGGCCAGCAGCTTTTGAGCTCTTGTGAGCGCGCGCGAGGGGC 1394
Qy 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
Db 1395 TGTCGCGTATGTTGCTGGCTATACAAGAGGTGTCAGCATCATTTGGGACCATGTTTCAG 1454
Qy 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
Db 1455 TGCTTCGAC-----TGGAAATTGGCAGATGTTTCGGGCAATAT 1493
Qy 489 ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
Db 1494 GTGGACATGACCGAAGCGTCTGGATTGACCGCTCCGAGAGCGTTTCGATCTGTTTGGCGG 1553
Qy 509 ProLeuAlaArgIleGlyValAlaSer 517
Db 1554 TTGTATCCAGGGTTGACCGGCCACA 1580

RESULT 3
US-09-672-785-1
; Sequence 1, Application US/09672785
; Patent NO. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masaaki
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229

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Db	799	-AGTTTGAGGGGGGTGGTGGTGAGAGGGGTGAGAGGTGAAGGAT--TTTITGGATAT	854
QY	275	rLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile***	295
Db	855	GTITGTTGGATGTGATCGAGAGTGAGAAATCGGAGGTGGAGTTTACGAGGAGCATCTCAA	914
QY	295	*GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTr	315
Db	915	AGCTTTTGATTGGATTCTTCTTCACTCCGGTACAGACACAACAGCAATCACAACAGAAATG	974
QY	315	pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty	335
Db	975	GGCAATATGACAGAACTCATTTAGCAATCCAAATGTACTCAAAAAGAGCTCAAGAAGATGGA	1034
QY	335	rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTvril	355
Db	1035	CAAAAGTCATAGGATCACAAGGTTGTTCAGAAATCCGACGCCCTTACTTGCCTTACCT	1094
QY	355	eArgAlaIleValLysGluThrPheArgMethisProProLeuProValValLysArgLys	375
Db	1095	CAACGCGATCATAAAAGAAACGTTTCGTCTCCACCTCCAAATCCCATGCTCACTAGAAA	1154
QY	375	sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph	395
Db	1155	ATCAATTTCTGACGTTGTGGTCAACGGGTACACGATCCCTGCCAAAACGCTATTGTTGT	1214
QY	395	eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr	415
Db	1215	CAACCTTTTGTCTCCTCGGGAAGAAATCTTACTACTCGGAAAATCCGATGAGTTCGACC	1274
QY	415	oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly**	435
Db	1275	CGAGAGGTTTCTCGAAAGGG-----ACCGGTGCGATAGACGTTAAAGGGCA	1322
QY	435	*HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl	455
Db	1323	GCATTTTCGAGTTGCTCCCGTTTGCGACGCGGCGGCGGTGCGCGGGATGTTGTAGG	1382
QY	455	aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValle	475
Db	1383	CATGACGAGGTGTTTAGTATTATCCGGGCTATGGTGCAGTGCCTTCATTTGGAAACTG--	1440
QY	475	uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl	495
Db	1441	----CCCGATGGTGTG-----AAGTCGGTCGACATGACCGGCGGCC	1478
QY	495	aglyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle	513
Db	1479	CGGGTTTGACGGCTCCACGTGCGCAATGATTGTTGTGCCAATTTGGTGCACCGGATT	1533

RESULT 4

US-09-672-785-7

; Sequence 7, Application US/09672785

; Patent No. 6596927

; GENERAL INFORMATION:

; APPLICANT: Mizutani, Masako

; APPLICANT: Kasumi, Masaaki

; APPLICANT: Ayabe, Shin-ichi

; APPLICANT: Akashi, Tomoyoshi

; TITLE OF INVENTION: Genes Coding for Flavone Synthases

; FILE REFERENCE: 001560-383

; CURRENT APPLICATION NUMBER: US/09/672,785

; CURRENT FILING DATE: 2000-09-29

; PRIORITY APPLICATION NUMBER: PCT/JP00/04379

; PRIORITY FILING DATE: 2000-01-30

; PRIORITY APPLICATION NUMBER: PCT/JP00/00490

; PRIORITY FILING DATE: 1999-01-28

; PRIORITY APPLICATION NUMBER: JP 11-205229

; PRIORITY FILING DATE: 1999-01-19

; PRIORITY APPLICATION NUMBER: JP 11-22427

; PRIORITY FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Perilla frutescens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-09-672-785-7

Alignment Scores:
Pred. No.: 3.54e-117 Length: 1770
Score: 921.50 Matches: 190
Percent Similarity: 57.46% Conservative: 91
Best Local Similarity: 38.85% Mismatches: 183
Query Match: 38.57% Indels: 25
DB: 4 Gaps: 8

US-09-857-581B-66 (1-521) x US-09-672-785-7 (1-1770)

Qy 33 ProAsnProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
Db 99 CCTACCTCCCGCGCGTTCCTCTCTCCATCATCGGCCACTTACACTCTCTCGG 155
Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer 72
Db 156 CCGAGA---CTCCACCAACCTTCCAGATCTGTCCCAACGGTACGGGCCCTTAATGCAG 212
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Db 213 CTCCGCTCGCGGTCCATCGCTGCTCATTCCTGCTGCTCGCGGAGCTCGCCAGGAATGC 272
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Db 273 CTCAAGACACAGAGCTGCTC---TTCTCTCCCGCAACACTCCACGGCCATGATATC 329
Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg 132
Db 330 GTCACTACGATTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 389
Qy 133 LysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg 152
Db 390 AAATATGACCTACGAGCTCTCGCGCGCGGAAATCTCGCCCATCTTCAGCCCATCAGG 449
Qy 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
Db 450 ACTCTGAAGTCAAGTCTTTCTCCAAATCTTATGCGCAAGGGTGAATCGGGGGAGC 509
Qy 173 LeuAsp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu 192
Db 510 TTCAACGTGACTGAGAGCTGTGAGCTGACGAGCAACGTCATATCGCATATGATGCTG 569
Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204
Db 570 AGCATACGGTGTTCAGACACGAGTTCGAGGCGGAGCGCGGAGCGGCGGATGATTCGGGAG 629
Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 630 GTCAACGATATTTGGGAGTTCGAGCTCTCCGACATCATATGCTTGTGTAAGAACTTC 689
Qy 225 LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal 244
Db 690 GATTTCAGGTATAGGAACGGTCCGAGATATCCAGAGATATGATGCTCTGCTG 749
Qy 245 GluArgValIleLysLysLysArg***IleValArgArgArg***AsnGlyGlu***** 264
Db 750 GAGAAGATCATCCGACACAGAGAGAAG-----CAGAGCGGACCCACGGCGGGTGGC 803
Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284
Db 804 GCGCGCGGGAAGCAAGGATTTCTTGACATGTTCTCTCGACATATGAGAGCGGGA 863
Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304

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Db 864 GCCGAAGTTAAATTCACGAGGGAGCATCTCAAAGCTTTGATTCTGGATTTCTTCCAGCC 923
Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
Db 924 GGCACCCAGACGAGCGGCGATCGTGTGTGAATGGCGGATAGCAGAGATGATCAACAATCCA 983
Qy 325 ***ValLeu*****AlaArgGluGlu***TySerValValGlyLysAsp***LeuVal 344
Db 984 AATGTGTGAAGAAAGCTCAAGAGAGATTCGCCAACATCTCGGATTCGACAGATTCGTG 1043
Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
Db 1044 CAAGAATCCGACGCCCAATCTGCCCTTACCTTCAAGCCCTCATCAAGAAACATTCGG 1103
Qy 365 MetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
Db 1104 CTCACCTCCAAATCCCAATGCTGGCGAGAAATCGATCTCCGACTCGCTCATCGAGCGC 1163
Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404
Db 1164 TACATGATTCCGCCAACACACGCTCTCTTCTGTCACCTCTGTCCTCGGCGGAGACCT 1223
Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
Db 1224 AAAATCTGGGACTTACCAGCGCGCTTCCAGCGGAGAGGTTTCTGGAGAAG----- 1274
Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
Db 1275 ---GAAAGGCGCGCATCGATGTTAAAGGGCAGCATTTTGGCTGCTACCGTTCCGAAC 1331
Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
Db 1332 GGCAGGAGAGCTGCCCGAGGATGCTTTTACCATTCAGAGGTGTCATCATTAATTGGG 1391
Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
Db 1392 ACGATGATTCAATGCTTCGATTGGAAGCTG-----CCCGACGCG----- 1430
Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
Db 1431 ---TCCGCGCATGTTGATATGGCAGAAACGGCGGCTCAGCGCACCGGAGACCGAT 1487
Qy 505 LeuValCysValProLeuAlaArgIle 513
Db 1488 TTGTTTTCGCTGTGGTGGCGCGGATT 1514

RESULT 5
US-09-142-108C-16
; Sequence 16, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Brugnolera, Filippa
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142.108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: P8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Chrysanthemum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1530)
US-09-142-108C-16

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Alignment Scores:

Pred. No.: 8,12e-78 Length: 1660
 Score: 637.50 Matches: 162
 Percent Similarity: 49.81% Conservative: 101
 Best Local Similarity: 30.68% Mismatches: 208
 Query Match: 26.68% Indels: 57
 DB: 4 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-142-108C-16 (1-1660)

Qy 5 LeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro***Ala 24
 Db. 34 CTCATCTCGGG---TCAGTACTATGTTTCTTAACCTA-----72
 Qy 25 ***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro-----Arg 41
 Db 73 AGTTTCAGTAATCCGCGACACTCCACCGCGGCAACACCATGGCCCTATAGTCGGGAAC 132
 Qy 42 LeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuHisTyrAla***Ile 61
 Db 133 TTACCACACCTTGGC-----CCATCCACACGACACTCGCG 171
 Qy 62 AspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrVal 81
 Db 172 GCCTTAGCCAAAGAGTACCGGCGCCATTGATCACCCTCGGCTCGGTGTGGACGTGGTT 231
 Qy 82 ValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe 101
 Db 232 GTGCCCGCGTCTGTCCTGAGTGCACAGTTTAAAGTTTACGACGCA---AATTTT 288
 Qy 102 ***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla 120
 Db 289 GCTAGTAGCGCGCAAAATCTGGCGCAACATGTGCGGTATATATACAGTCTGTG 348
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140
 Db 349 TTGACACTTATGCTCCAGGTGCGGTGTTGTAAGGAAGATTGTTGCGTCCATTTGTT 408
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 409 TCTGCTAAAGACTTGATGATTTTTCATGTCATGTCAGGAGGAGGTAGCGTCTTAACC 468
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 469 CGGTACTACTGAGTGTGGAACCTCA-----CGGTACAGCTTGGCCAACTACTTAAC 522
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGly-----193
 Db 523 GTGTGTGCCCAACACCGCTTAGCACGCGGTAAATGTAGTAGAGAGAGTTCGCGAGACGGA 582
 Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***Gly 210
 Db 583 ATTGACAGGTGACCGCAATGAGTTCAAAGATAGGTAGTAGAGTAATGTTAGTATAGCAGGA 642
 Qy 211 GlutY-SerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGlu 230
 Db 643 GAATTTAACCTTGGTGACTTATTCCTGTACTTGCACCTTACCTACGACGACATTA 702
 Qy 231 LysArgIleAspIleLeuAsnLysPheAspProValGluArgValIleLysLys 250
 Db 703 AAAAAAATGAAGAGCTTCATGTTGCGTTCGATTCATTTCTTAGTAAGATCGTTGAGGAG 762
 Qy 251 ArgArg***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGly 270
 Db 763 CATAAACG-----GCACCTGGTGGGTGGTGGTCACTACT 795
 Qy 271 Val***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***Glu---IleLysIle 289
 Db 796 GATTTGCTGACGAGCTTGATTTTACCTTAAGATGATGCTCATATTGAGTGGGAGCTT 855
 Qy 290 ThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThr 309
 Db 856 ACAGATACTGAATCAAGCTTTGCTTCTGAATTTATTCGTCGCGGAACACAGACATCC 915

Qy 310 Ala*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu***** 329
 Db 916 TCTAGTACAGTAGAATGGGCAATAGCGCACTCATTCGTCTCCACAAATATTAAACAA 975
 Qy 330 AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr 349
 Db 976 GCCCGAGAGAGATAGACGCTGTAGTTGGTCAAGACCGGCTTTAAACAGAAATGGACTTG 1035
 Qy 350 GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeu 369
 Db 1036 AGCCAACTAACATACCTCCAGGCTCTTGTGAAGAGGTGTTAGGCTCCACCCCTTCAACG 1095
 Qy 370 ProVal---ValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
 Db 1096 CCATCTCTCTTACCAAGATATCATCCGAGAGTGTGAGGTGATGGTATATATCCCT 1155
 Qy 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
 Db 1156 AAGGGATCCACACTCTCTCGTTAACGTGTGGCCATTGCGCGAGACCCAAAAATGTGGCG 1215
 Qy 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
 Db 1216 GATCCTCTTGAATTTAGGCTTCTCGGTTTTTA-----CCCGGGGAGAAAGCC 1266
 Qy 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
 Db 1267 GTGCTGATGTAGGGGAATGATTTGAAGTTATACCATTTGGGCGAGCAAGGATT 1326
 Qy 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
 Db 1327 TGTGCGGTATGACGCTAGGCTTGAGATCGTCCAGTGTCTCATTCGACATTGGTCCAA 1386
 Qy 469 CysPheAspLeuGlnVal-----LeuGlyProGlnGlyGlnIleLeuLysGly*** 485
 Db 1387 ACTTTTCAITGGGAACCTGCGTACCGGTTAGACCGGAG-----1425
 Qy 486 AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeu 505
 Db 1426 -----ATGCTCAACATGAAGAAGCGTATGGATTCACCTTCAACGGGTGCACCCCTTG 1479
 Qy 506 ValCysValProLeuAlaArgIle 513
 Db 1480 ATGTTTCAACCGAAGCCGAGGTTA 1503

RESULT 6

US-09-689-783A-1
 ; Sequence 1, Application US/09689783A
 ; Patent No. 6605469
 ; GENERAL INFORMATION:
 ; APPLICANT: KANG, JEONG-CU
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A CYTOCHROME P450 HYDROXYLASE IN
 ; FILE OF INVENTION: BRASSINOSTEROID BIOSYNTHESIS IN PLANTS
 ; FILE REFERENCE: 107572
 ; CURRENT APPLICATION NUMBER: US/09/689,783A
 ; CURRENT FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1488
 ; TYPE: DNA
 ; ORGANISM: Pisum sativum
 ; US-09-689-783A-1

Alignment Scores:
 Pred. No.: 1.03e-76 Length: 1488
 Score: 629.00 Matches: 154
 Percent Similarity: 49.79% Conservative: 87
 Best Local Similarity: 31.82% Mismatches: 199
 Query Match: 26.33% Indels: 44
 DB: 4 Gaps: 12

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US-09-857-581B-66 (1-521) x US-09-689-783A-1 (1-1488)
Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 106 CCACGAGGCCCAAAACCA---TGGCCCAATAATAGCAAACTTCAACCTTATT---GGAACC 159
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 160 CTCCACCAACCAATCCCTCCATGGGCTCACCACAAATATGGACCTATTATGCATCTATGG 219
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 220 TTGGCTCCAAACCGCTGCTGGCTCACTGTAGAAATGGCAAGCCCTTCTCAAA 279
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 280 ACCCAGCAGCAACG---TTAGCCGGCGGACCCAAATTCCTGCGGAAATAACACAAC 336
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 337 TATAACTACTCTGACATAAATCTGTCTCAGTACGCTCGCTATTTGGCGCAAGCTCGGAGA 396
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 397 ATGTGCTCTATTAGAAATGTTTGTAGTCAAAACGCTCTGAGCTTATGATGATCAATGAAGAA 456
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 457 CAAGAGTTACATGTTTTTTTACATGAATCTTTGATTTCTAGAAAC-----AAACAATT 510
Qy 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
Db 511 TTGTTGAAGACCACTCTTCAAGTTTGAGTCTAAATGTTATAGTAGAATGGTCTTAGGA 570
Qy 194 -----GluAlaGluGluIleArgAspIle 201
Db 571 AGAAATATCTAGAGAAGTTGAAATCTTATATTTCTCCGGATGAGTTTAAAGATTG 630
Qy 202 AlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeu 221
Db 631 TTGGATGAGTTGTTTTCCTTAATGGGATCTTAAATATGGGATTTTATTCCTTGAT 690
Qy 222 Lys***LeuLysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAsp 241
Db 691 CATTTCTTAGATTTTCAAGGGTATGTGAAGAGTGAAGGTTTTCAGTAAAGATTTGAT 750
Qy 242 ProValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 261
Db 751 GGATTTATGGAACATGTGTTGGAGGAACAT-----ATTGAAGAAGAAAGGTTTAAAG 804
Qy 262 Glu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGlu 281
Db 805 GATTATGTTGCTAGGAT-----ATGGTGGATGTTCTTTGCACTTGTCTGAG 852
Qy 282 AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp*** 301
Db 853 GATCCTGATCTTGAAGTCAAACTTGAAGACATGGTGTAAAGCTTTTACTCAGGACTTG 912
Qy 302 PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIle 321
Db 913 ATAGCAGGAGGACAGAGAGCTGTACAGTAGAATGGCAATCTCAGAGCTTAATA 972
Qy 322 AsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp 341
Db 973 AGAAACCAAGAAATCTTCAAGAAAGCAACAGAGAACTAGACAGATTAATAGGAAGAGAA 1032
Qy 342 ***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGlu 361
Db 1033 AGATGGGTTGAAGAGAAAGACATTTCTAATCTACCTTATGTTTATGCAATTTGCTTAAAGAA 1092
Qy 362 ThrPheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys 380
Db 1093 ACAATGAGACTTCACCCAGTGGCCCAATGTTTAGTACCAGAGAAGAGCTAGAGAAGATTGC 1152
```

RESULT 7

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US-09-142-108C-5
; Sequence 5, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Bruggliera, Filipina
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142,108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PN8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(1629)
US-09-142-108C-5
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Alignment Scores:
Pred. No.: 3.35e-76 Length: 1711
Score: 626.00 Matches: 162
Percent Similarity: 47.94% Conservative: 94
Best Local Similarity: 30.34% Mismatches: 216
Query Match: 26.20% Indels: 62
DB: 4 Gaps: 14
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US-09-857-581B-66 (1-521) x US-09-142-108C-5 (1-1711)

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Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db 145 TTATTGTGGCATGTACTTTTATATAGGGTCTTGTCTTATATATCTTCTCTC----- 198
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro***Pro 40
Db 199 -----AAACAAAAGTAAGCACTGCCCTCGACCAAGCCATGGCCC 243
```

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Qy 41 -----ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHis 57
Db 244 ATCTCGGAATCTGCCACATCTTGGCCGAGGCC-----CAC 282
Qy 58 TyrAla***IleAspLeuSerLysLysGlyHisGlyProLeuPheSer*****PheGlySer 77
Db 283 CAGTCGATGGCGCGCTGGCAGCGGTGCAGCGCCATTAATCTCTGAAGATGGGCTTT 342
Qy 78 MetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****Glu 97
Db 343 GTGCATGTGGTGTGGCTCTCTAGCATCGCTGGGAGAAATTTCTGAAGGTGCATGAC 402
Qy 98 AlaThrSerPhe***ThrArgPheGlnThr.SerAla***Arg***LeuThrThrAsp--- 116
Db 403 GCA---AATCTCTCGAGCAGCGCTCCCAATTCGGGTGCAAAACACGTCGGCTACAACTAT 459
Qy 117 *****ValAla*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMet 136
Db 460 CAGGACTTGGTCTTGTCTCTATGGCCCGCTGGCGGATGCTCAGCAAAATCTGTGCA 519
Qy 137 AsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIle 156
Db 520 CTCACCTCTCTCCGCCAAAGCCTTGAACGACTTCACACGTCACAGGATGAGGTG 579
Qy 157 ArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***Thr 176
Db 580 GGGATCTCTACTCGCTTCTAGCAGATCGAGGAAACG-----CCGTTGAATTAGGG 633
Qy 177 GluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
Db 634 CAGATGATGAACACATCGGCCCAACCAATGCAATGCGGTGTATGTGGTTCGACGGGTG 693
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLys 207
Db 694 GTTGGCAGCAGACTCAAAAGCGGAGAGTTAAAGCAATGGTGTAGTGGATGGTA 753
Qy 208 Ile***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 754 TTAGCTGGTGTGTCACTTAGGTGATTTATCCACCTCTTGAAAAATTGGATCTCAA 813
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPhe 240
Db 814 GGTGTCTATGTAAGATGAAGAAGCTTCACTTGGTTCGACTCGTCTCTTGGTGAAG--- 870
Qy 241 AspProValValGluArgValIleLysLysArg***IleValArgArgArg***Asn 260
Db 871 -----ATCCTTGGAGACCAAGATC 891
Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db 892 AACAGCTCAGATGAACCAAGGCCATTCGGATTTGTGAACATGTTAATTTCTTTGAAG 951
Qy 281 Glu---AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValVal 299
Db 952 GAGCTGATGATGCGGAAGGAGGAGGCTCACCGACGTAGAAATTAAGCGGTGCTCTG 1011
Qy 300 Asp***PheSerAlaGly***AspSerThrAla*****ThrGluTTrpAlaLeuAlaGlu 319
Db 1012 AACTGTTTCTGTCAGAGACTGACACAACTCAAGCACTGTGGAATGGTGCATGCTGAG 1071
Qy 320 LeuIleAsnAsnPro*****ValLeu*****AlaArgGluGlu***TyrSerValValGly 339
Db 1072 TTAGTAGCAGATCTGGAATCTTCCCAAGATGCCAAAGAACCTCGACTCTGTGTGGT 1131
Qy 340 LysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleVal 359
Db 1132 AAGAAATCGGTGTGAAGGAGGTGATCTGCGCGGATTAACCATTCCTCCAAGCGGTGTC 1191
Qy 360 LysGluThrPheArgMetHisProProLeuProVal---ValLysArgLysCys***Glu 378
Db 1192 AAGAAATTTCCGACTCCATCTCTCCACCCCGCTCTCCCTACCGAGATCGCACATGAG 1251
Qy 379 GluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrp 398

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Db 1252 AGTTGTGAAGTGAATGATACTTGAATTCAAAGGGTTCGACACTTCTTGTCAATGTTGG 1311
Qy 399 GlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPhe 418
Db 1312 GCAATGTCTCGCATCAAAATGTGTGGATGAACCACTAGAGTTCCGGCTGAACGATTC 1371
Qy 419 LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438
Db 1372 TTGAAG-----GGCGGGGAAAGCCCTAAATGTCTGATGTTAGAGGAAATGATTTCGAA 1422
Qy 439 LeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly 458
Db 1423 TTGATACCGTTCGGAGCGGCGGCGAAGAAATTTGTGCAGGAATGAGCTTAGGAATACGTATG 1482
Qy 459 ***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGln 478
Db 1483 GTCAGTGTGTGACAGCAACTTTGAACCACTGCGTTTGACTTTTGATTTG-----GCGGAT 1536
Qy 479 GlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThr 498
Db 1537 GGACAGTTG-----CTGAAAGCTTAAACATGGAGGAAGCTTATGGGCTGACC 1584
Qy 499 ValProArgAlaHisSerLeuValCysValProLeuAlaArg 512
Db 1585 TTGCAACGAGTCAACCTTTGGTAGTCACCCCGAAGCCTAGG 1626

RESULT 8
US-09-499-302A-1
; Sequence 1, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; TITLE OF INVENTION: INCOMPATIBLE INTERACTION
; FILE REFERENCE: 10324/P64443USO
; CURRENT APPLICATION NUMBER: US/09/499, 302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-499-302A-1

Alignment Scores:
Pred. No.: 4,92e-76 Length: 1781
Score: 625.00 Matches: 151
Percent Similarity: 49.28% Conservative: 89
Best Local Similarity: 31.01% Mismatches: 211
Query Match: 26.16% Indels: 36
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-499-302A-1 (1-1781)
Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeu-----Lys 52
Db 100 CTTCTGTGTCATGG---AAATTTACCTTTTATTGGAAGCCTACATCACTTGGCAGTGCCA 156
Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 157 GTTCCACTTCTCTCATCATCATCGCTTAAATAATCTAGCAAAACTTTATGGCGCGCTCATGCAC 216
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Db 217 TTACGACTCGGGAATTTCTACCGTCATCATTTCTCCCGCGAATGGGAAGGAATA 276
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Db 277 CTAAAAAATCAGCAGC---CTCGCTTTTCGCAACGAGGCCGAAACTTGTGTGGTGTGATC 333

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Db 212 AAGTACGGCGGTGGCGGACGTGCAGCTGGGAGAGTACTCGGTGGTCTCTCTCG 271
Qy 86 ProGluLeuPheLeuLeuGln*****GluAlaThrSerPhe*****ThrArgPhe 105
Db 272 GCGGAGCAGCGAAGCAGCGAGCGATGAAGGTGTGAC---CCGAACTTCGCGCAGCGGTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyrAsp---*****ValAla*****Pro*** 124
Db 329 GACGGCATCGGTCCAGGACCATGTGTACACAAAGATGACATCATCTTCAGCCCTTAC 388
Qy 125 GlyProTyrTrp****PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaThrThr 144
Db 389 AACGATCACTGGCGCCAGATCGCGAGGATCTGCGTACAGAGCTGCTGAGCCCGAAGAAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 449 GTCAGGTCTTCGGGTATACATAAGCAGCAGAGATCAGCGCCTCATCCGGCTGCTCGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTyr***Asn 184
Db 509 TCCTCGGGGGAGCG---CCGTCGACGTACCGGAGGAGGTGTCGAAGATGTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Db 563 GTCGTCTGTGTCAGCGCGCGTTCGGGAGTGTCTCAAGGACCGAGGTTCGTTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db 623 TTGTTGAAGGAGTTCGCTGCACTTCGCGGTTCGAGCTGCGGAT---CTCTACCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
Db 680 TCCTCATGCTCTCAACCTGCTTAGCTTGAAACAAGTAC-----AGTTGCGAGAGATG 733
Qy 237 LeuAsnLysPheAspProValGluArgValIleLysLysArgArg***IleValArg 256
Db 734 CGCGCGCGCTCGATCATCATCTTGATGGTTCCTGGAGGAGCATAGG-----781
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
Db 782 -----GAGAAGAAGAGCGCGCGAGTTGGAGCGGAGGACATCGTCGACGTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
Db 827 CTTTTCAGGTGAGAGAGCGGCGGACATCAAAATTCCTTCAATTCATTCATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Db 887 GGTTTCATTTTCGACACCTTCTCGCGGAGCTGAAACGTCCTTCGACGACCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Db 947 GCGTTGTGCGAACTGTATGAGAAATCCGCGAAGATGCCAAGGTGCGGCGGAGTAAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
Db 1007 GAGCGCTCAAGGAAGACAGCTGTGGATTGAGCGAGGTGCAAGCTTAAATACCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Db 1067 AGATCGGTGTAAAGGAGACTCTGAGGCTGCACCTCCCTTCTCCATTATCCCAAGACAA 1126
Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Db 1127 TCAGGGAAGAAATGCGAGGTAAACGGGTACACGATTCGCGCCAAAATAAGAAATCTTCATC 1186
Qy 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
Db 1187 AAGCTGTGGCTATCGAAGGGATCCCATATCTGGAAGATCCCGACACCTTCCGCCCT 1246
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
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Db 1247 GAGGATTCGATGAGGTTCACAG-----GATTTTCATGGGAAC 1285
Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db 1286 GATTCGAGTTCATCCCATTCGGGGGGGTGGAAGAATCTGCCCGGTTTACATTTCCGG 1345
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Db 1346 CTGGCAATGTTGAGATCCCATTTGGCGCAACTCTCTACCACTTCGACTCGGAATTTG--- 1402
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
Db 1403 ---CCACAAGGATG-----ACTGATGCCACTTGGACATGACGGAGACCCCA 1447
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db 1448 GGTCTTTCTGGGCGCAAAAGAAATGTTTGTGTTGTTCC 1489

RESULT 12
US-09-292-768-65
; Sequence 65, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; LIPONIC ACID: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1762)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: spearmint limonene-6-hydroxylase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
; US-09-292-768-65

Alignment Scores:
Pred. No.: 3,86e-75 Length: 1762
Score: 618.50 Matches: 146
Percent Similarity: 48.38% Conservative: 93
Best Local Similarity: 29.55% Mismatches: 214
Query Match: 25.89% Indels: 41
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-292-768-65 (1-1762)

Qy 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
Db 101 TCGAAATCCAAACCAACCTA-----CCTCGAGGCCT---CCGAAGCTGCCGGTATC 151
Qy 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Db 152 GGCACCTCCACTCTCTGTTGGGAGGCTTCCCGACGACGTGTTAGGAGCATAGCCAG 211
Qy 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
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Db 212 AAGTACGGGCGGTGGCGCAGCTGCTGAGGAAAGTGTACTCGGTGGTGTCTGCTGCTG 271
Qy 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 272 GCGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyArgPhe*****ValAla*****Pro*** 124
Db 329 GACGGCATCGGGTCCAGGACCATGTGTGTACGACAAAGATGAGATCATCTTCAGCCCTTAC 388
Qy 125 GlyProTyTrp***PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaThrThr 144
Db 389 AAGCATCAGTGGCGCCAGATGCGGAGGATCTGCTGACAGAGCTGTGAGCCCGGAGAAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnLeuArgLys***LeuArg***MetAla 164
Db 449 GTCAGGTCTTCGGGTACATAAGCAGGAGGAGATCGAGCGCCTCATCCGGCTGCTCGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp***Asn 184
Db 509 TCGTGGGGGGGAGCG-----CGGTGACGTGACGAGGAGGTGTGCAAGATGTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluLeuArgAsp 200
Db 563 GTGTCTGTGTCAGGGCGGCGGTTCGGGAGGTGTCTCAAGGACGAGGTTCTGTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTySerLeuThrAspPheIle***Pro 220
Db 623 TTGGTGAAGAGTCTGTGGCATTTGGCTCGGGTTGAGCTGGCGGAT---CTCTACCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyGlyLysArgIleAspAspIle 236
Db 680 TCCTCATGGTCTCTCAACCTGCTTAGCTTGAACAAGTAC-----AGGTTGCAGAGGATG 733
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 734 CGCGCGCGCTCATCATCTTGTGAGTGTCTGAGGAGGATAGG-----781
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
Db 782 -----GAGAGAGAGAGCGGCGAGTTTGGAGCGGAGGAGCATCTGTCGAGCTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
Db 827 CTTTTCAGGATGCAAGAGGCGAGCATCAAAATTCCTTACTTCCATTTGATTCATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Db 887 GGTTCATTTTCGACACCTTTCTCGCGGAGGAGTGAACGCTTTCGACGACCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Db 947 CGGTGTGCGACTGATGAGATCCGCGCAAGATGCCAAGTGGCGAGGAGGTGAAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyTrpIle 355
Db 1007 GAGCGCTCAAGGAAAGACAGTCTGATTTGAGCGAGGTGCAAGACTAAAATACTCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Db 1067 AGATCGGTGTAAAGGAGACTCTGAGGCTGCACCCCTCTTCCATTAATCCCAAGACAA 1126
Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Db 1127 TCAGGGAAGATCGGAGTTACGGGTACAGATTCCGGCCAAACTAGAACTTTCATC 1186
Qy 396 AsnValTrpGlnValGly*****Asp***LysTyTrpAspArgProSerGlu***ArgPro 415
Db 1187 AACGTCTGGGTATCGGAGGATCCCACTATCTGGGAAGATCCGACACCTTCGCGCCT 1246
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
Db 1247 GAGAGATTCGATGAGGTTTCCAGG-----GATTTCATGGGAAAC 1285
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Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db 1286 GATTCGAGTTTCATCCATTCGGGGCGGTGCGAAGAATCTGCCCGGTTTACATTCGGG 1345
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Db 1346 CTGGCAAAATGTTGAGATCCCATTTGGCGCAACTCTCTTACCACTTCGACTCGAAATTG--- 1402
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
Db 1403 ---CCACAGGAATG-----ACTGATGCCGACTTGGACATGCGGAGACCCCA 1447
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db 1448 GGTCTTCTGGGCCAAAGAAAAAATGTTGTGTTGTTCCC 1489
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RESULT 13

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US-09-351-229-3
; Sequence 3, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; EARLIER FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Zea mays
US-09-351-229-3
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Alignment Scores:
Pred. No.: 4-7e-75 Length: 1806
Score: 618.00 Matches: 164
Percent Similarity: 50.40% Conservative: 90
Best Local Similarity: 32.54% Mismatches: 199
Query Match: 25.87% Indels: 52
DB: 3 Gaps: 13
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US-09-857-581B-66 (1-521) x US-09-351-229-3 (1-1806)

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Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 86 CGCGCGGCGCCCAAGCCA---TGGCCGATCATCGCAACCTTAACCTCATG---GGCGAG 139
Qy 55 LeuLeuHisTyTrpAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 140 CTCCCGCCACCGCTCCCAATGAACGAGCTCTCCAAAGCGGTACGGTCCGCTCATGCTCTGG 199
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 200 TTCGGGTGCTGTGCTGTGTGCTGCGCGGTCCGCCGAGATGCGCAAGCTCTTCTCAAG 259
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 260 ACCAACGACGCG---GCGTTCTCCGACCGCGCGAGGTTCCAGTCCGCAAGACACCGCG 316
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyTrp***PheValArgLys 133
Db 317 TACGACTGCTCCGCGCTTCTGTGGGTCTCTTTGAGCGCTACCTGCGCCAGGACGCGAGG 376
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 377 ATCTGGCGCCACCGAGCTCTTCAGCGCCACCGCGGTCTCGAGTCTCTCGAGCATCCCGGAC 436
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
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Db 241 CTCGGCAGGAGTTCCTCGCTGCTCTCCGCGCGAGGCCAGAGGAGCGCATGAAG 300
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 301 CTGGTGGAC---CCGGCTCGCGGACCGGTTCGAGAGCATCGGAGCAGAGATCATGTGG 357
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 358 TACGACACACGACGACATCATCTTCAGGCCCTTACAGCGTGCACATCGCGCCAGATCGCGAAG 417
Qy 134 LeuileMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGCGTCTCCGAGCTCCTCAGCGCCGCGAACCTCCGCTCTTCGGCTTCATCAGGCAG 477
Qy 154 GlnGlnileArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTGTCGCCCTCCTCGGCACCTCGCTCCGCTCCGCGCGCGGGGAGCGCGTG 537
Qy 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGGAGCGGATGACGACGCTGACGTGCTCCATCATCTGCAGGCGCGCTTCGGG 597
Qy 194 -----GluAlaGluGluileArgAspIleAlaArgGluValLeuLysIle*** 209
Db 598 AGCGTGATCAGGACCGACGAGAGCTGGTGAGCTGGTGAAGGAGCGCCCTCAGCATGGCG 657
Qy 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 658 TCCGGGTTCGAGCTCGCGGACATGTTCCCTCTCCAGCTCCTCAACTGCTCTGCTGG 717
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
Db 718 AACAAAGCAAGCTGTGGAGGATCGCGCGCGCTGCAGCGCATCTCTCGAGGCCATC--- 774
Qy 242 ProValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 261
Db 775 ---GTGAGGAGCAACAAGCTCAAGAG----- 798
Qy 262 Glu*****GluGlyGlu***SerGlyVal---***LeuAspThrLeuLeuGluPheAla 280
Db 799 -----AGCGCGAGTTGGCGGCGGAGACATATTGACGTACTCTTAGGATCGAG 849
Qy 281 GluAspGluThr***GluileLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db 850 AAGGATAGCCAGATCAAAAGTCCCATCACCACCAAGCCATCAAGCGCTTCATCTTCGAC 909
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 910 ACGTTCCTCAGCGGGGACCGAGACATCATCAACCACCCCTGTGGTGGTGGCGGAGCTG 969
Qy 321 IleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLys 340
Db 970 ATGAGGAATCAGAGGTGATGGCGAAGCGCGGAGGTGAGAGCGCGCTGAAAGGGG 1029
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACCGACTCGGAGCTGGAGCGAGCTGCAGGAGCTTAAGTACATGAATCGGTGTGAAG 1089
Qy 361 GluThrPheArgMetHisProProLeuProValLysArgLysCys***GluGluCys 380
Db 1090 GAGACGATGAGGATGACCCCTCCGATCCCGTTGATCCGAGATCATCGAGATCATGAGAGAATGC 1149
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGGTCAACGGGTACAGATTCGGAATAGCCGAGATCATGATCAACGTTGTGCTCCAT 1209
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GTTAGGAATCCTCTACTTGGGAAACCCGAGACCTTTGGCCCGAAGGTTT----- 1263
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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Db 1264 -----GACCAAGTCTCAGGAGATTTCATGTGGAAACGATTTTCAGATTTCATC 1308
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1309 CCATTTGGAGCTGGAAGAAGATCTGCCCGGTTTGAATTTCCGGTTTGGCAATGTTGAG 1368
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db 1369 GTCCATTGGCACAGCTTCTTACCACCTTCGACTTGGGAAGTTGGCGGAAGGAATGAACCT 1428
Qy 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluAlaGlyLeu 497
Db 1429 -----TCCGATATGACATGTCTGAGGCGAAGGCGCTT 1461
Qy 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAGAAGAACAATCTTCTACTCGTTCCT 1497

RESULT 15
US-09-292-768-3
; Sequence 3, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: waur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Mentha piperita
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
; US-09-292-768-3

Alignment Scores:
Pred. No.: 6 69e-75 Length: 1665
Score: 616.50 Matches: 145
Percent Similarity: 47.76% Conservative: 90
Best Local Similarity: 29.47% Mismatches: 206
Query Match: 25.81% Indels: 51
DB: 3 Gaps: 11

US-09-857-581B-66 (1-521) x US-09-292-768-3 (1-1665)
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Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 181 CTCCCGCAGCACGCGTGGCCAGCGTGCAGGAGCAGTACGCGCCAGTACGCGCCAGTCGACG 240
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 241 CTGCGCGAGGTGTCTCCGTCGTCTCTCCGCGGAGGCCAGGAGGCGGATGAAG 300
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 301 CTGGTGGAC---CCGGCTCGCGGACCGGTTCGAGAGCATCGGAGCAGATCATGTGG 357
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 358 TACGACACACGACGACATCATCTTTCAGCCCTTACAGCGTGCATCTGCGCGCAGATCGCGAAG 417
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Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGCGTCTCCGAGCTCTCAGCGCCGCAACCTCCGCTCTCTTCGCTTTCATCAGGCAG 477
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTGTCCTCCGCTCTCCGCTCTCCGCTCTCCGCTCTCCGCTCTCCGCTCTCCGCT 537
Qy 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGGAGCGGATAGCGACGCTGACGCTGCTCCATCATCTGACGCGCGGCTTCGGG 597
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle*** 209
Db 598 AGCGTGATCAGGAGCACCGAGGAGCTGGTGAGCTGGTGAGGAGCGCCCTCAGCATGGCG 657
Qy 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 658 TCCGGGTTCGAGCTCGCGGACATGTTCCCTCTCCCAAGCTCTCACTTGTCTGCTGG 717
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
Db 718 AACAGAGCAAGCTGTGGAGGATGCGCGCGGCTCGACGCCATCTCTCGAGGCCATC--- 774
Qy 242 ProValValGluArgValIleLysLysArgArg***IleValArgArg***AsnGly 261
Db 775 ---GTGAGGAGCACAAGCTCAAGAAG----- 798
Qy 262 Glu*****GluGlyGlu***SerGlyVal---LeuAspThrLeuLeuGluPheAla 280
Db 799 -----ACGCGGAGTTTGGCGGAGGACATATTGACGTACTCTTTAGGATCCAG 849
Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db 850 AAGGATAGCCAGATCAAGTCCCATCCACCAACGCCATCAAGGCCCTTCACTCTTCGAC 909
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 910 ACGTTCTACGGGGACCGAGACATCATCAACACACCTGTGGGTGATGGCGGAGCTG 969
Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
Db 970 ATGAGGAATCCAGAGGTGATGGCGAAGCGCAGCGAGGTGAGCGCGCTGAAGGGG 1029
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACCGACTGGGACGTGGACGACGTGACGAGCTTAAGTACATGAATCGTGTGAAG 1089
Qy 361 GluThrPheArgMetHisProLeuProValValLysArgLysCys***GluGluCys 380
Db 1090 GAGACGATGAGGATGACCCCTCCGATCCCGTGTATCCCGAGATCATGCAAGGTGCTCCATG 1149
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGGTCAACGGGTACAGATTCCGAATAAGCCAGAAATCATGATCAACGTGTGCTCCATG 1209
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GTTAGGAATCCTCTCTACTCGGAAAAACCCGAGACCTTTTGGCCCGAAAGGTTT----- 1263
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1264 -----GACCAGTCTCGAGGATTTTCATGGAAACGATTTTCGATTCATC 1308
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1309 CCATTTGGAGCTGGAAGAAGATCTGCCCGGTTTGAATTCGGGTGGCAATGTTGAG 1368
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db 1369 GTCCCATTTGGCAGCTTCTTTACCTTCGACTCGAAGTTGGCGGAAGGAATGAACCTT 1428
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Qy 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
Db 1429 -----TCCGATATGGACATGTCTGAGGCGAAGGCCTT 1461
Qy 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAAGAAAGAACATCTTCTACTCGTTCCC 1497
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